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## OM protein - protein search, using sw model

Run on: May 17, 2005, 10:15:05 ; Search time 23 Seconds

(Without alignments)  
759,473 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195  
Sequence: 1 MNTLPEDMENALTGSSQSHS.....EAGSEAEKQDEKPLEL 234Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7469064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.4	55.6	445	2	US-08-691-8148-6
2	85.5	7.2	449	2	US-09-949-016-8594
3	82.5	6.9	341	2	US-08-846-762-92
4	80.5	6.7	350	4	US-09-489-039A-9711
5	79.5	6.7	406	4	US-09-171-639-6
6	79.5	6.7	406	5	PCT-US94-02107-2
7	79.5	6.7	723	4	US-09-976-594-503
8	78.5	6.6	221	4	US-09-270-767-11033
9	78.5	6.6	221	4	US-09-270-767-56249
10	78.5	6.6	766	4	US-09-724-653-2
11	78.5	6.6	766	4	US-09-724-653-14
12	78.5	6.6	766	4	US-09-724-653-15
13	78.5	6.5	228	4	US-08-248-796A-20444
14	78.5	6.5	251	4	US-09-270-767-43373
15	78.5	6.5	355	4	US-08-833-752-9
16	78.5	6.5	355	4	US-09-938-719-9
17	78.5	6.5	355	4	US-09-939-226B-9
18	78.5	6.4	353	2	US-08-466-103A-14
19	77.7	6.4	353	3	US-09-280-420-2
20	77.7	6.4	353	3	US-09-479-195-2
21	76.5	6.4	435	4	US-09-489-039A-12344
22	76.5	6.4	494	1	US-08-464-340A-4
23	76.5	6.4	494	5	PCT-US94-0849A-4
24	76.5	6.4	195	4	US-09-134-000C-5592
25	75.5	6.4	593	4	US-09-720-317A-22
26	75.5	6.3	263	4	US-09-583-110-3148
27	75.5	6.3	264	4	US-09-107-433-4877

28	75.5	6.3	352	4	US-09-492-709A-293	Sequence 293, App
29	75.5	6.3	355	4	US-09-248-796A-14258	Sequence 14258, A
30	75.5	6.3	397	4	US-09-721-870-105	Sequence 105, App
31	75.5	6.3	433	4	US-09-721-870-107	Sequence 107, App
32	75.5	6.3	471	2	US-08-477-451-20	Sequence 20, App
33	75.5	6.3	499	4	US-09-721-870-40	Sequence 40, App
34	75.5	6.3	467	4	US-09-328-352-5465	Sequence 5465, Ap
35	75.5	6.3	549	4	US-09-134-000C-4375	Sequence 4375, Ap
36	74.5	6.2	355	1	US-08-153-848-28	Sequence 28, App
37	74.5	6.2	355	1	US-08-153-848-32	Sequence 32, App
38	74.5	6.2	355	3	US-09-299-843A-28	Sequence 28, App
39	74.5	6.2	355	3	US-09-299-843A-32	Sequence 32, App
40	74.5	6.2	355	3	US-09-088-337B-28	Sequence 28, App
41	74.5	6.2	355	3	US-09-088-337B-32	Sequence 32, App
42	74.5	6.2	355	4	US-09-170-496D-130	Sequence 130, App
43	74.5	6.2	355	4	US-09-170-496D-232	Sequence 232, App
44	74.5	6.2	355	4	US-09-917-254-68	Sequence 68, App
45	74.5	6.2	355	5	PCT-US93-11153-28	Sequence 28, App
46	74.5	6.2	355	5	PCT-US93-11153-32	Sequence 32, App
47	74.5	6.2	471	1	US-07-996-772A-11	Sequence 11, App
48	74.5	6.2	471	3	US-09-032-742-2	Sequence 2, App
49	74.5	6.2	471	3	US-09-032-742-11	Sequence 11, App
50	74.5	6.2	471	3	US-09-032-742-14	Sequence 14, App
51	74.5	6.2	471	3	US-09-032-742-17	Sequence 17, App
52	74.5	6.2	471	3	US-09-145-864-4	Sequence 4, App
53	74.5	6.2	940	4	US-09-328-352-8165	Sequence 8165, Ap
54	74.5	6.2	154	4	US-09-543-681A-7579	Sequence 7579, Ap
55	74.5	6.2	332	4	US-09-107-433-2662	Sequence 2662, Ap
56	74.5	6.2	332	2	US-08-466-103A-12	Sequence 12, App
57	74.5	6.2	333	2	US-08-896-365-6	Sequence 6, App
58	74.5	6.2	680	4	US-09-248-796A-15089	Sequence 15089, A
59	73.5	6.2	312	4	US-09-543-681A-6267	Sequence 6267, Ap
60	73.5	6.2	400	4	US-09-902-540-11488	Sequence 11488, A
61	73.5	6.2	3033	1	US-07-925-695-9	Sequence 9, App
62	73.5	6.2	199	4	US-09-107-532-6773	Sequence 6773, Ap
63	73.5	6.1	212	4	US-09-903-456-75	Sequence 75, App
64	73.5	6.1	364	3	US-09-077-675A-16	Sequence 16, App
65	73.5	6.1	364	4	US-09-077-675A-16	Sequence 16, App
66	73.5	6.1	364	4	US-09-762-651A-6	Sequence 6, App
67	73.5	6.1	364	4	US-09-743-875-3	Sequence 3, App
68	73.5	6.1	377	3	US-09-743-875-5	Sequence 5, App
69	73.5	6.1	494	4	US-09-949-016-7475	Sequence 7475, Ap
70	73.5	6.1	501	4	US-09-489-039A-9817	Sequence 9817, Ap
71	73.5	6.1	746	2	US-08-785-431-4	Sequence 4, App
72	73.5	6.1	746	3	US-09-205-048-4	Sequence 4, App
73	73.5	6.1	788	3	US-08-785-431-2	Sequence 2, App
74	73.5	6.1	312	4	US-09-205-048-2	Sequence 2, App
75	73.5	6.1	353	4	US-09-248-796A-20385	Sequence 20385, A
76	72.5	6.1	353	4	US-09-134-000C-5562	Sequence 5562, Ap
77	72.5	6.1	359	4	US-09-134-000C-5442	Sequence 5442, Ap
78	72.5	6.1	448	2	US-08-811-897A-16	Sequence 16, App
79	72.5	6.1	448	2	US-08-811-897A-16	Sequence 16, App
80	72.5	6.1	448	3	US-08-855-213-16	Sequence 16, App
81	72.5	6.1	448	3	US-09-201-474-16	Sequence 16, App
82	72.5	6.1	476	2	US-08-811-897A-14	Sequence 14, App
83	72.5	6.1	476	2	US-08-855-213-14	Sequence 14, App
84	72.5	6.1	476	3	US-09-201-474-14	Sequence 14, App
85	72.5	6.1	445	2	US-08-811-897A-17	Sequence 17, App
86	72.5	6.1	445	2	US-08-855-213-17	Sequence 17, App
87	72.5	6.1	445	3	US-09-201-474-17	Sequence 17, App
88	72.5	6.1	513	2	US-08-811-897A-15	Sequence 15, App
89	72.5	6.1	513	2	US-08-855-213-15	Sequence 15, App
90	72.5	6.1	513	3	US-09-201-474-15	Sequence 15, App
91	72.5	6.1	673	4	US-09-949-016-7656	Sequence 7656, Ap
92	72.5	6.0	666	4	US-09-949-016-6546	Sequence 6546, Ap
93	72.5	6.0	741	4	US-09-585-858-11	Sequence 11, App
94	72.5	6.0	741	4	US-10-270-878-11	Sequence 11, App
95	72.5	6.0	1038	4	US-09-388-092-487	Sequence 487, App
96	72.5	6.0	2307	3	US-09-263-933-9	Sequence 2, App
97	72.5	6.0	2307	3	US-09-263-933-9	Sequence 2, App
98	72.5	6.0	2307	3	US-09-263-933-16	Sequence 16, App
99	72.5	6.0	2307	4	US-09-919-901-2	Sequence 2, App
100	72.5	6.0	2307	4	US-09-919-901-9	Sequence 9, App

101	72	6.0	2307	4	US-09-919-901-16	Sequence 16, Appl	174	70	5.9	333	4	US-09-170-496D-16	Sequence 16, Appl
102	72	6.0	2307	4	US-10-191-966-2	Sequence 2, Appl	175	70	5.9	338	4	US-09-170-496D-172	Sequence 172, App
103	72	6.0	2307	4	US-10-191-966-9	Sequence 9, Appl	176	70	5.9	333	4	US-09-248-796A-17918	Sequence 17918, A
104	72	6.0	2307	4	US-10-191-966-16	Sequence 16, Appl	177	70	5.9	361	4	US-09-270-767-40072	Sequence 40072, A
105	71.5	6.0	342	3	US-08-785-928-1	Sequence 1, Appl	178	70	5.9	361	4	US-09-270-767-55288	Sequence 55288, A
106	71.5	6.0	342	3	US-08-728-603-17	Sequence 17, Appl	179	70	5.9	359	4	US-09-248-796A-16608	Sequence 16608, A
107	71.5	6.0	366	2	US-08-466-103A-4	Sequence 4, Appl	180	70	5.9	412	4	US-09-248-796A-22404	Sequence 22404, A
108	71.5	6.0	366	2	US-08-896-365-7	Sequence 7, Appl	181	70	5.9	425	4	US-09-107-532A-6574	Sequence 6574, Ap
109	71.5	6.0	382	4	US-09-262-477-2	Sequence 2, Appl	182	70	5.9	470	4	US-09-328-352-5397	Sequence 5397, Ap
110	71.5	6.0	510	4	US-09-679-686B-19	Sequence 19, Appl	183	70	5.9	471	3	US-09-328-314-17	Sequence 17, Appl
111	71.5	6.0	670	4	US-09-575-081B-26	Sequence 26, Appl	184	70	5.9	757	4	US-09-540-236-2346	Sequence 2346, Ap
112	71.5	6.0	724	4	US-09-949-016-10086	Sequence 10086, A	185	70	5.8	188	4	US-09-328-352-4951	Sequence 4951, Ap
113	71	5.9	312	1	US-08-118-270-98	Sequence 38, Appl	186	69.5	5.8	270	4	US-09-252-991A-29192	Sequence 29192, A
114	71	5.9	312	5	PCT-US93-08528-38	Sequence 38, Appl	187	69.5	5.8	321	4	US-09-198-452A-778	Sequence 778, App
115	71	5.9	423	5	US-09-540-236-2988	Sequence 25, Appl	188	69.5	5.8	321	4	US-09-168-019-2	Sequence 2, Appl
116	71	5.9	470	3	US-09-292-071-85	Sequence 25, Appl	189	69.5	5.8	382	4	US-09-169-205D-21	Sequence 21, Appl
117	71	5.9	470	3	US-09-292-069A-25	Sequence 25, Appl	190	69.5	5.8	453	4	US-09-583-110-3842	Sequence 3842, Ap
118	71	5.9	470	3	US-09-767-013-65	Sequence 25, Appl	191	69.5	5.8	461	4	US-09-107-433-3722	Sequence 3722, Ap
119	71	5.9	470	4	US-09-292-072-25	Sequence 8, Appl	192	69.5	5.8	454	4	US-09-489-039A-8154	Sequence 8154, Ap
120	71	5.9	471	1	US-07-817-920-8	Sequence 8, Appl	193	69.5	5.8	557	4	US-10-327-189-4	Sequence 4, Appl
121	71	5.9	471	1	US-08-370-542-7	Sequence 8, Appl	194	69.5	5.8	557	4	US-09-521-195B-3	Sequence 3, Appl
122	71	5.9	471	1	US-08-117-006-8	Sequence 8, Appl	195	69.5	5.8	557	4	US-09-798-743-1	Sequence 1, Appl
123	71	5.9	471	1	US-08-216-59A-8	Sequence 8, Appl	196	69.5	5.8	557	4	US-09-949-016-6309	Sequence 6309, Ap
124	71	5.9	471	1	US-08-342-358-7	Sequence 7, Appl	197	69.5	5.8	558	4	US-09-438-185A-792	Sequence 792, App
125	71	5.9	471	2	US-08-244-434-2	Sequence 2, Appl	198	69.5	5.8	559	4	US-09-328-352-5924	Sequence 5924, App
126	71	5.9	471	3	US-09-018-351-7	Sequence 7, Appl	199	69.5	5.8	559	4	US-09-489-039A-9425	Sequence 9425, Ap
127	71	5.9	471	3	US-09-032-742-8	Sequence 8, Appl	200	69.5	5.8	599	1	US-08-301-722A-5	Sequence 5, Appl
128	71	5.9	471	3	US-09-145-864-2	Sequence 2, Appl	201	69.5	5.8	610	4	US-09-949-016-7929	Sequence 7929, Ap
129	71	5.9	471	4	US-09-170-496D-122	Sequence 122, App	202	69.5	5.8	660	3	US-09-134-001C-5039	Sequence 5039, Ap
130	71	5.9	471	4	US-09-170-496D-228	Sequence 228, App	203	69.5	5.8	663	3	US-08-559-004-5	Sequence 5, Appl
131	71	5.9	471	5	US-10-092-138A-28	Sequence 28, Appl	204	69.5	5.8	676	4	US-09-949-016-9494	Sequence 9494, Ap
132	71	5.9	471	5	PCT-US93-00149-8	Sequence 8, Appl	205	69.5	5.8	877	4	US-09-165-396-5	Sequence 5, Appl
133	71	5.9	2296	3	US-08-286-819A-27	Sequence 27, Appl	206	69.5	5.8	1088	4	US-09-328-352-5749	Sequence 5749, Ap
134	71	5.9	2296	3	US-08-980-357-87	Sequence 27, Appl	207	69.5	5.8	1684	3	US-08-665-259-25	Sequence 25, Appl
135	70.5	5.9	228	3	US-09-291-922-16	Sequence 16, Appl	208	69.5	5.8	1684	3	US-08-762-500-75	Sequence 25, Appl
136	70.5	5.9	297	4	US-09-328-352-7074	Sequence 7074, Ap	209	69.5	5.8	1704	4	US-09-032-438C-110	Sequence 120, App
137	70.5	5.9	365	3	US-08-155-005A-8	Sequence 8, Appl	210	69.5	5.8	1766	4	US-09-949-016-10796	Sequence 10796, A
138	70.5	5.9	365	3	US-09-363-783-8	Sequence 8, Appl	211	69.5	5.8	193	3	US-08-858-207A-430	Sequence 430, App
139	70.5	5.9	365	4	US-09-661-758A-8	Sequence 8, Appl	212	69	5.8	340	4	US-09-248-796A-15237	Sequence 15237, A
140	70.5	5.9	367	4	US-09-543-681A-4643	Sequence 4643, Ap	213	69	5.8	370	3	US-08-513-974B-26	Sequence 26, Appl
141	70.5	5.9	379	1	US-08-118-270-32	Sequence 32, Appl	214	69	5.8	370	3	US-08-513-974B-333	Sequence 323, App
142	70.5	5.9	379	5	PCT-US93-08528-32	Sequence 32, Appl	215	69	5.8	370	3	US-09-172-353-5	Sequence 5, Appl
143	70.5	5.9	388	3	US-08-155-005A-6	Sequence 6, Appl	216	69	5.8	370	3	US-08-776-971-21	Sequence 21, Appl
144	70.5	5.9	388	3	US-09-363-783-6	Sequence 6, Appl	217	69	5.8	370	3	US-08-776-971-104	Sequence 104, App
145	70.5	5.9	388	4	US-09-661-758A-6	Sequence 6, Appl	218	69	5.8	370	4	US-09-799-955-5	Sequence 5, Appl
146	70.5	5.9	390	3	US-08-155-005A-4	Sequence 4, Appl	219	69	5.8	370	4	US-09-461-436B-26	Sequence 26, Appl
147	70.5	5.9	390	3	US-08-155-005A-17	Sequence 17, Appl	220	69	5.8	370	4	US-09-576-290-21	Sequence 21, Appl
148	70.5	5.9	390	3	US-09-363-783-4	Sequence 4, Appl	221	69	5.8	370	4	US-09-576-290-104	Sequence 104, App
149	70.5	5.9	390	4	US-09-661-758A-17	Sequence 17, Appl	222	69	5.8	388	4	US-09-492-709A-378	Sequence 378, App
150	70.5	5.9	390	4	US-09-661-758A-4	Sequence 4, Appl	223	69	5.8	422	4	US-09-489-039A-8418	Sequence 8418, Ap
151	70.5	5.9	499	3	US-09-134-001C-5370	Sequence 5370, Ap	224	69	5.8	552	4	US-09-270-767-445540	Sequence 445540, A
152	70.5	5.9	539	3	US-09-291-922-86	Sequence 26, Appl	225	69	5.8	661	4	US-09-543-681A-5453	Sequence 5453, Ap
153	70.5	5.9	539	1	US-07-879-617A-10	Sequence 10, Appl	226	69	5.8	661	4	US-09-248-796A-20857	Sequence 20857, A
154	70.5	5.9	539	1	US-08-295-814E-11	Sequence 11, Appl	227	69	5.8	725	4	US-09-489-039A-20849	Sequence 20849, A
155	70.5	5.9	539	1	US-08-753-985-10	Sequence 10, Appl	228	69	5.8	139	4	US-09-270-767-36588	Sequence 36588, A
156	70.5	5.9	539	3	US-09-084-813-4	Sequence 4, Appl	229	68.5	5.7	139	4	US-09-134-000C-37174	Sequence 37174, Ap
157	70.5	5.9	599	3	US-09-343-361-11	Sequence 11, Appl	230	68.5	5.7	199	3	US-08-478-316-36	Sequence 36, Appl
158	70.5	5.9	599	5	PCT-US92-09662-4	Sequence 4, Appl	231	68.5	5.7	199	3	US-09-019-792A-36	Sequence 36, Appl
159	70.5	5.9	1027	2	US-08-551-437-2	Sequence 2, Appl	232	68.5	5.7	200	4	US-09-601-326-36	Sequence 36, Appl
160	70.5	5.9	1027	3	US-09-004-225-2	Sequence 2, Appl	233	68.5	5.7	225	4	US-09-543-681A-7698	Sequence 7698, Ap
161	70.5	5.9	1027	3	US-09-084-346-2	Sequence 2, Appl	234	68.5	5.7	257	2	US-08-996-365-8	Sequence 8, Appl
162	70.5	5.9	1027	3	US-09-084-346-2	Sequence 2, Appl	235	68.5	5.7	257	2	US-09-448-796A-20728	Sequence 20728, A
163	70.5	5.9	1027	3	US-09-104-704-2	Sequence 2, Appl	236	68.5	5.7	257	2	US-09-161-994A-12	Sequence 12, Appl
164	70.5	5.9	1027	1	US-08-769-309A-5	Sequence 5, Appl	237	68.5	5.7	327	3	US-09-542-733-2	Sequence 2, Appl
165	70.5	5.9	1780	3	US-08-994-570-5	Sequence 5, Appl	238	68.5	5.7	362	3	US-08-196-989B-4	Sequence 4, Appl
166	70.5	5.9	1781	4	US-09-961-403-13	Sequence 13, Appl	239	68.5	5.7	363	1	US-08-760-936-4	Sequence 4, Appl
167	70.5	5.9	1481	4	US-09-248-796A-27134	Sequence 27134, A	240	68.5	5.7	383	2	US-09-125-024-4	Sequence 4, Appl
168	70	5.9	153	2	US-08-896-365-9	Sequence 9, Appl	241	68.5	5.7	383	2	US-09-134-000C-5002	Sequence 5002, Ap
169	70	5.9	298	4	US-09-270-767-34605	Sequence 34605, A	242	68.5	5.7	437	4	US-08-466-103A-2	Sequence 2, Appl
170	70	5.9	298	4	US-09-563-110-5003	Sequence 5003, Ap	243	68.5	5.7	437	4	US-09-328-352-5102	Sequence 5102, Ap
171	70	5.9	307	4	US-08-148-215A-4	Sequence 4, Appl	244	68.5	5.7	444	3		
172	70	5.9	307	4			245	68.5	5.7				
173	70	5.9	333	1			246	68.5	5.7				

247	68.5	5.7	444	4	US-09-580-734-15	Sequence 15, Appl	320	68	5.7	472	4	US-09-951-217-36	Sequence 36, Appl
248	68.5	5.7	444	4	US-08-374-009-15	Sequence 15, Appl	321	68	5.7	480	1	US-08-440-103-22	Sequence 22, Appl
249	68.5	5.7	444	4	US-09-131-724-15	Sequence 15, Appl	322	68	5.7	480	1	US-08-440-542-22	Sequence 22, Appl
250	68.5	5.7	444	4	US-09-631-603-11	Sequence 11, Appl	323	68	5.7	480	1	US-08-231-568-22	Sequence 22, Appl
251	68.5	5.7	448	2	US-08-811-897A-22	Sequence 22, Appl	324	68	5.7	480	1	US-08-440-210-22	Sequence 22, Appl
252	68.5	5.7	448	2	US-08-855-213-22	Sequence 22, Appl	325	68	5.7	480	3	US-09-046-604-22	Sequence 2, Appl
253	68.5	5.7	448	3	US-09-201-474-22	Sequence 22, Appl	326	68	5.7	488	1	US-08-115-365-2	Sequence 2, Appl
254	68.5	5.7	468	4	US-09-631-603-19	Sequence 19, Appl	327	68	5.7	488	1	US-08-586-897-2	Sequence 2, Appl
255	68.5	5.7	468	4	US-09-826-509-553	Sequence 553, App	328	68	5.7	488	4	US-09-826-509-561	Sequence 561, App
256	68.5	5.7	475	2	US-08-811-897A-26	Sequence 26, Appl	329	68	5.7	503	1	US-08-484-840-4	Sequence 4, Appl
257	68.5	5.7	475	2	US-08-855-213-26	Sequence 26, Appl	330	68	5.7	503	1	US-08-484-840-4	Sequence 4, Appl
258	68.5	5.7	475	3	US-09-201-474-26	Sequence 26, Appl	331	68	5.7	727	5	US-08-424-424B-2	Sequence 2, Appl
259	68.5	5.7	476	2	US-08-811-897A-24	Sequence 24, Appl	332	68	5.7	727	5	PCT-US94-05362A-2	Sequence 2, Appl
260	68.5	5.7	476	2	US-08-811-897A-28	Sequence 28, Appl	333	68	5.7	859	4	US-09-538-092-206	Sequence 206, App
261	68.5	5.7	476	2	US-08-855-213-24	Sequence 24, Appl	334	68	5.7	908	3	US-08-823-110-1	Sequence 1, Appl
262	68.5	5.7	476	2	US-08-855-213-28	Sequence 28, Appl	335	68	5.7	908	3	US-08-604-298-1	Sequence 1, Appl
263	68.5	5.7	476	3	US-09-201-474-24	Sequence 24, Appl	336	68	5.7	968	3	US-08-551-999A-7	Sequence 7, Appl
264	68.5	5.7	476	3	US-09-201-474-28	Sequence 28, Appl	337	68	5.7	968	3	US-09-385-752-7	Sequence 7, Appl
265	68.5	5.7	525	2	US-08-811-897A-23	Sequence 23, Appl	338	68	5.7	968	4	US-09-949-016-5914	Sequence 5914, Ap
266	68.5	5.7	525	2	US-08-855-213-23	Sequence 23, Appl	339	68	5.7	987	4	US-09-949-016-10368	Sequence 10368, A
267	68.5	5.7	535	3	US-09-201-474-23	Sequence 23, Appl	340	68	5.7	2013	1	US-08-324-977-12	Sequence 12, Appl
268	68.5	5.7	538	4	US-09-149-476-469	Sequence 469, App	341	68	5.7	2013	2	US-08-384-616-12	Sequence 12, Appl
269	68.5	5.7	552	2	US-08-811-897A-27	Sequence 27, Appl	342	68	5.7	2013	2	US-08-304-686A-12	Sequence 12, Appl
270	68.5	5.7	552	2	US-08-855-213-27	Sequence 27, Appl	343	68	5.7	2013	3	US-09-315-850-12	Sequence 12, Appl
271	68.5	5.7	552	2	US-09-201-474-27	Sequence 27, Appl	344	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
272	68.5	5.7	553	2	US-08-811-897A-25	Sequence 25, Appl	345	68	5.7	2620	2	US-08-384-616-32	Sequence 32, Appl
273	68.5	5.7	553	2	US-08-811-897A-29	Sequence 29, Appl	346	68	5.7	2620	2	US-08-304-686A-32	Sequence 32, Appl
274	68.5	5.7	553	2	US-08-855-213-25	Sequence 25, Appl	347	68	5.7	2620	3	US-09-315-850-32	Sequence 32, Appl
275	68.5	5.7	553	2	US-08-855-213-29	Sequence 29, Appl	348	68	5.7	2621	1	US-08-324-977-36	Sequence 36, Appl
276	68.5	5.7	553	3	US-09-201-474-25	Sequence 25, Appl	349	68	5.7	2621	2	US-08-384-616-36	Sequence 36, Appl
277	68.5	5.7	553	3	US-09-201-474-29	Sequence 29, Appl	350	68	5.7	2621	2	US-08-304-686A-36	Sequence 36, Appl
278	68.5	5.7	570	4	US-09-949-016-8907	Sequence 8907, Ap	351	68	5.7	3010	3	US-09-315-850-36	Sequence 36, Appl
279	68.5	5.7	660	4	US-09-252-991A-29685	Sequence 29685, A	352	68	5.7	3010	1	US-08-324-977-2	Sequence 2, Appl
280	68.5	5.7	738	4	US-09-107-532A-5096	Sequence 5096, Ap	353	68	5.7	3010	1	US-08-324-977-14	Sequence 14, Appl
281	68.5	5.7	762	4	US-09-724-653-7	Sequence 7, Appl	354	68	5.7	3010	2	US-08-384-616-2	Sequence 2, Appl
282	68.5	5.7	1296	4	US-09-462-136-9	Sequence 9, Appl	355	68	5.7	3010	2	US-08-384-616-14	Sequence 14, Appl
283	68	5.7	188	4	US-09-270-767-36930	Sequence 36930, A	356	68	5.7	3010	2	US-08-304-686A-2	Sequence 2, Appl
284	68	5.7	188	4	US-09-270-767-52147	Sequence 52147, A	357	68	5.7	3010	2	US-08-304-686A-14	Sequence 14, Appl
285	68	5.7	247	4	US-09-603-208A-152	Sequence 152, App	358	68	5.7	3010	3	US-09-315-850-2	Sequence 2, Appl
286	68	5.7	258	3	US-09-053-197A-7	Sequence 7, Appl	359	68	5.7	3010	3	US-09-315-850-14	Sequence 14, Appl
287	68	5.7	309	4	US-09-085-761A-7	Sequence 7, Appl	360	67.5	5.6	210	4	US-09-248-796A-20156	Sequence 20156, A
288	68	5.7	355	4	US-09-328-352-5344	Sequence 6344, Ap	361	67.5	5.6	253	4	US-09-540-236-3093	Sequence 3093, Ap
289	68	5.7	355	4	US-09-585-876-2	Sequence 2, Appl	362	67.5	5.6	306	4	US-09-252-991A-32161	Sequence 32161, A
290	68	5.7	355	1	US-08-012-898A-2	Sequence 2, Appl	363	67.5	5.6	350	2	US-08-966-316-16	Sequence 16, Appl
291	68	5.7	355	1	US-08-450-393A-5	Sequence 5, Appl	364	67.5	5.6	350	4	US-09-721-908-2	Sequence 2, Appl
292	68	5.7	355	3	US-08-446-669-5	Sequence 5, Appl	365	67.5	5.6	330	4	US-09-721-941-12	Sequence 2, Appl
293	68	5.7	355	4	US-09-239-938-1	Sequence 1, Appl	366	67.5	5.6	457	4	US-09-543-681A-6044	Sequence 6044, Ap
294	68	5.7	355	4	US-09-886-319A-14	Sequence 14, Appl	367	67.5	5.6	459	4	US-09-594-519-3	Sequence 3, Appl
295	68	5.7	355	4	US-10-039-659A-13	Sequence 13, Appl	368	67.5	5.6	489	4	US-09-694-519-8	Sequence 8, Appl
296	68	5.7	355	4	US-09-961-068-1	Sequence 1, Appl	369	67.5	5.6	515	4	US-09-869-433-2	Sequence 2, Appl
297	68	5.7	355	4	US-09-625-573-5	Sequence 5, Appl	370	67.5	5.6	554	4	US-09-198-452A-369	Sequence 369, App
298	68	5.7	355	4	US-09-960-547-1	Sequence 1, Appl	371	67.5	5.6	546	4	US-09-358-185A-353	Sequence 353, App
299	68	5.7	355	5	PCT-US95-00476-5	Sequence 7048, Ap	372	67.5	5.6	546	4	US-09-252-991A-17104	Sequence 17104, A
300	68	5.7	373	4	US-09-107-532A-7048	Sequence 7048, Ap	373	67.5	5.6	865	4	US-09-252-991A-16683	Sequence 16683, A
301	68	5.7	414	4	US-09-489-039A-10869	Sequence 10869, A	374	67.5	5.6	1234	2	US-08-811-897A-56	Sequence 56, Appl
302	68	5.7	426	4	US-09-486-192-2	Sequence 2, Appl	375	67.5	5.6	1324	3	US-09-201-474-56	Sequence 56, Appl
303	68	5.7	471	3	US-08-492-459-14	Sequence 14, Appl	376	67.5	5.6	1411	4	US-09-338-092-413	Sequence 413, App
304	68	5.7	471	3	US-08-423-752-14	Sequence 14, Appl	377	67.5	5.6	2158	4	US-10-144-198-34	Sequence 34, Appl
305	68	5.7	471	3	US-08-716-873-8	Sequence 8, Appl	378	67.5	5.6	2265	4	US-10-144-198-35	Sequence 35, Appl
306	68	5.7	471	3	US-08-716-873-8	Sequence 8, Appl	379	67.5	5.6	2318	3	US-09-091-219-24	Sequence 24, Appl
307	68	5.7	471	3	US-09-368-431-8	Sequence 8, Appl	380	67.5	5.6	2318	4	US-09-660-541-24	Sequence 24, Appl
308	68	5.7	471	3	US-09-368-431-18	Sequence 18, Appl	381	67.5	5.6	2697	4	US-10-144-198-12	Sequence 12, Appl
309	68	5.7	471	3	US-09-414-006-14	Sequence 14, Appl	382	67.5	5.6	153	4	US-09-198-452A-329	Sequence 329, App
310	68	5.7	471	4	US-09-447-223-14	Sequence 14, Appl	383	67	5.6	153	4	US-09-338-092-413	Sequence 413, App
311	68	5.7	471	4	US-09-951-217-8	Sequence 8, Appl	384	67	5.6	159	4	US-09-134-185A-314	Sequence 314, Appl
312	68	5.7	471	4	US-09-951-217-8	Sequence 8, Appl	385	67	5.6	159	4	US-09-302-540-13804	Sequence 13804, A
313	68	5.7	472	4	US-09-792-024-68	Sequence 89, Appl	386	67	5.6	199	3	US-08-478-316-32	Sequence 32, Appl
314	68	5.7	472	3	US-08-492-459-22	Sequence 22, Appl	387	67	5.6	199	3	US-09-019-793A-32	Sequence 32, Appl
315	68	5.7	472	3	US-08-423-752-22	Sequence 22, Appl	388	67	5.6	200	4	US-08-131-628A-11	Sequence 11, Appl
316	68	5.7	472	3	US-08-716-873-36	Sequence 36, Appl	389	67	5.6	200	4	US-08-301-435-15	Sequence 15, Appl
317	68	5.7	472	3	US-09-368-431-36	Sequence 36, Appl	390	67	5.6	200	4	US-09-601-326-32	Sequence 32, Appl
318	68	5.7	472	3	US-09-414-006-22	Sequence 22, Appl	391	67	5.6	200	5	PCT-US95-10904-15	Sequence 15, Appl
319	68	5.7	472	4	US-09-447-223-22	Sequence 22, Appl	392	67	5.6	200	5	PCT-US95-10904-15	Sequence 15, Appl

393	67	5.6	207	4	US-08-811-519-26	Sequence 26, App1	466	66.5	5.6	849	4	US-09-949-016-8846	Sequence 8846, Ap
394	67	5.6	272	4	US-09-270-767-37728	Sequence 37728, A	467	66.5	5.6	849	4	US-09-949-016-8847	Sequence 8847, Ap
395	67	5.6	272	4	US-09-270-767-52945	Sequence 52945, A	468	66.5	5.6	853	4	US-09-949-016-8275	Sequence 8275, Ap
396	67	5.6	282	4	US-09-270-767-35735	Sequence 35735, A	469	66.5	5.6	853	4	US-09-949-016-8276	Sequence 8276, Ap
397	67	5.6	282	4	US-09-270-767-50952	Sequence 50952, A	470	66.5	5.6	977	4	US-09-134-000C-5553	Sequence 5553, Ap
398	67	5.6	295	3	US-09-372-422A-38	Sequence 38, App1	471	66.5	5.6	1897	4	US-09-792-024-98	Sequence 98, App1
399	67	5.6	360	4	US-09-107-532A-4523	Sequence 4523, Ap	472	66.5	5.6	2261	4	US-08-444-818-66	Sequence 66, App1
400	67	5.6	464	4	US-09-248-796A-18187	Sequence 18187, A	473	66.5	5.6	2894	2	US-08-466-975A-23	Sequence 23, App1
401	67	5.6	479	4	US-09-543-681A-6605	Sequence 6605, Ap	474	66.5	5.6	2894	3	US-08-391-671A-23	Sequence 23, App1
402	67	5.6	480	1	US-08-440-103-18	Sequence 18, App1	475	66.5	5.6	2894	3	US-08-467-902A-23	Sequence 23, App1
403	67	5.6	480	1	US-08-440-542-18	Sequence 18, App1	476	66.5	5.6	2894	4	US-09-375-265-23	Sequence 23, App1
404	67	5.6	480	1	US-08-231-368-18	Sequence 18, App1	477	66.5	5.6	2894	3	US-09-941-611-23	Sequence 23, App1
405	67	5.6	480	1	US-08-440-210-18	Sequence 18, App1	478	66.5	5.6	2955	2	US-08-443-260-3	Sequence 3, App1
406	67	5.6	480	3	US-09-046-604-18	Sequence 18, App1	479	66.5	5.6	2955	3	US-08-443-805A-3	Sequence 3, App1
407	67	5.6	496	4	US-10-146-704-3	Sequence 3, App1	480	66.5	5.6	2955	3	US-08-443-900A-3	Sequence 3, App1
408	67	5.6	733	4	US-09-489-039A-7885	Sequence 7885, Ap	481	66.5	5.6	2955	3	US-08-444-818-124	Sequence 124, App
409	67	5.6	978	4	US-09-585-858-50	Sequence 20, App1	482	66.5	5.6	2955	3	US-08-449-843-3	Sequence 3, App1
410	67	5.6	978	4	US-10-270-878-20	Sequence 20, App1	483	66.5	5.6	2995	3	US-08-444-818-138	Sequence 138, App
411	67	5.6	1093	4	US-09-248-796A-17108	Sequence 17108, A	484	66.5	5.6	3010	3	US-09-014-416A-3	Sequence 3, App1
412	67	5.6	1174	1	US-08-040-751-3	Sequence 3, App1	485	66.5	5.6	3011	1	US-08-440-103-36	Sequence 36, App1
413	67	5.6	1174	1	US-08-291-368-2	Sequence 2, App1	486	66.5	5.6	3011	1	US-08-440-542-36	Sequence 36, App1
414	67	5.6	1174	2	US-08-962-190-2	Sequence 2, App1	487	66.5	5.6	3011	1	US-07-910-760-10	Sequence 10, App1
415	67	5.6	1174	5	PCT-US95-10310-2	Sequence 2, App1	488	66.5	5.6	3011	1	US-08-440-519-10	Sequence 10, App1
416	67	5.6	1174	6	5164180-4	Patent No. 5164180	489	66.5	5.6	3011	1	US-08-231-368-36	Sequence 36, App1
417	67	5.6	1174	6	5164180-4	Patent No. 5164180	490	66.5	5.6	3011	1	US-08-440-210-36	Sequence 36, App1
418	67	5.6	1242	2	US-08-680-326-33	Sequence 33, App1	491	66.5	5.6	3011	2	US-08-433-678A-6	Sequence 6, App1
419	67	5.6	1242	4	US-09-904-065-12	Sequence 12, App1	492	66.5	5.6	3011	2	US-08-444-818-177	Sequence 17, App
420	67	5.6	1242	4	US-09-904-065-13	Sequence 13, App1	493	66.5	5.6	3011	3	US-09-014-416-5	Sequence 5, App1
421	67	5.6	3010	4	US-09-539-601-3	Sequence 3, App1	494	66.5	5.6	3011	3	US-08-529-169A-6	Sequence 6, App1
422	67	5.6	3010	4	US-09-539-601-21	Sequence 21, App1	495	66.5	5.6	3011	3	US-09-388-874-2	Sequence 2, App1
423	67	5.6	3010	4	US-09-539-601-27	Sequence 27, App1	496	66.5	5.6	3011	3	US-09-046-604-36	Sequence 36, App1
424	67	5.6	3010	4	US-09-539-601-53	Sequence 33, App1	497	66.5	5.6	3011	3	US-08-440-549-10	Sequence 10, App1
425	67	5.6	3287	2	US-08-477-451-7	Sequence 7, App1	498	66.5	5.6	3011	4	US-08-850-328-1	Sequence 1, App1
426	67	5.6	197	4	US-09-134-000C-4925	Sequence 4925, Ap	499	66.5	5.6	3011	4	US-09-483-799-6	Sequence 6, App1
427	66.5	5.6	200	3	US-08-686-968C-9	Sequence 9, App1	500	66.5	5.6	3011	5	US-09-916-359-2	Sequence 2, App1
428	66.5	5.6	243	2	US-09-328-352-7321	Sequence 7321, Ap	501	66.5	5.6	3011	5	PCT-US91-02228-10	Sequence 10, App1
429	66.5	5.6	288	2	US-08-466-103A-6	Sequence 6, App1	502	66	5.5	132	4	US-09-270-767-61535	Sequence 61535, A
430	66.5	5.6	289	4	US-09-248-796A-17919	Sequence 17919, A	503	66	5.5	219	4	US-09-248-796A-15621	Sequence 15621, A
431	66.5	5.6	293	4	US-09-248-796A-18278	Sequence 18278, A	504	66	5.5	282	4	US-09-107-532A-5717	Sequence 5717, Ap
432	66.5	5.6	341	4	US-09-248-796A-18985	Sequence 18985, A	505	66	5.5	289	3	US-09-134-001C-2917	Sequence 2917, Ap
433	66.5	5.6	345	3	US-09-291-922-14	Sequence 14, App1	506	66	5.5	302	4	US-09-107-532A-4973	Sequence 4973, Ap
434	66.5	5.6	359	4	US-09-828-523A-14	Sequence 14, App1	507	66	5.5	316	4	US-09-328-352-6692	Sequence 6692, Ap
435	66.5	5.6	370	4	US-09-828-523A-74	Sequence 74, App1	508	66	5.5	318	4	US-09-270-767-45996	Sequence 45996, A
436	66.5	5.6	384	4	US-09-949-016-6494	Sequence 6494, Ap	509	66	5.5	370	3	US-09-172-353-7	Sequence 7, App1
437	66.5	5.6	389	4	US-09-134-000C-3706	Sequence 3706, Ap	510	66	5.5	370	4	US-08-776-971-140	Sequence 140, App
438	66.5	5.6	397	4	US-09-902-540-13316	Sequence 13316, A	511	66	5.5	370	3	US-09-799-955-7	Sequence 7, App1
439	66.5	5.6	413	4	US-09-328-352-5589	Sequence 5589, Ap	512	66	5.5	370	4	US-09-576-290-140	Sequence 140, App
440	66.5	5.6	430	4	US-09-583-110-4230	Sequence 4230, Ap	513	66	5.5	381	2	US-08-845-566-3	Sequence 3, App1
441	66.5	5.6	437	4	US-09-107-433-3678	Sequence 3678, Ap	514	66	5.5	381	2	US-08-467-948A-28	Sequence 28, App1
442	66.5	5.6	454	3	US-08-444-818-73	Sequence 73, App1	515	66	5.5	381	3	US-08-852-824-18	Sequence 18, App1
443	66.5	5.6	468	4	US-09-248-796A-27314	Sequence 27314, A	516	66	5.5	381	3	US-08-467-947A-28	Sequence 28, App1
444	66.5	5.6	480	1	US-08-440-103-14	Sequence 14, App1	517	66	5.5	381	4	US-09-731-030A-17	Sequence 17, App1
445	66.5	5.6	480	1	US-08-440-542-14	Sequence 14, App1	518	66	5.5	381	5	PCT-US96-10618-4	Sequence 4, App1
446	66.5	5.6	480	1	US-08-231-368-14	Sequence 14, App1	519	66	5.5	405	4	US-09-799-978-38	Sequence 38, App1
447	66.5	5.6	480	1	US-08-440-210-14	Sequence 14, App1	520	66	5.5	412	4	US-10-138-701-59	Sequence 59, App1
448	66.5	5.6	480	3	US-09-046-604-14	Sequence 14, App1	521	66	5.5	433	4	US-09-134-000C-6536	Sequence 6536, Ap
449	66.5	5.6	537	4	US-09-489-039A-14149	Sequence 14149, A	522	66	5.5	447	4	US-09-825-923-2	Sequence 2, App1
450	66.5	5.6	550	1	US-08-121-057-4	Sequence 4, App1	523	66	5.5	450	4	US-09-825-923-4	Sequence 4, App1
451	66.5	5.6	550	2	US-08-509-187D-4	Sequence 4, App1	524	66	5.5	582	4	US-09-721-870-179	Sequence 179, App
452	66.5	5.6	550	2	US-09-121-396-4	Sequence 4, App1	525	66	5.5	583	4	US-09-270-767-38131	Sequence 38131, A
453	66.5	5.6	550	5	PCT-US93-03704A-4	Sequence 4, App1	526	66	5.5	583	4	US-09-270-767-53348	Sequence 53348, A
454	66.5	5.6	557	4	US-09-248-796A-15455	Sequence 15455, A	527	66	5.5	1230	4	US-08-938-291A-9	Sequence 9, App1
455	66.5	5.6	627	4	US-09-328-352-4917	Sequence 4917, Ap	528	66	5.5	1250	3	US-09-589-619-9	Sequence 9, App1
456	66.5	5.6	663	3	US-08-824-057-3	Sequence 3, App1	529	65.5	5.5	145	4	US-09-134-000C-3453	Sequence 3453, Ap
457	66.5	5.6	663	3	US-09-415-582-3	Sequence 3, App1	530	65.5	5.5	155	4	US-09-134-000C-3721	Sequence 3721, Ap
458	66.5	5.6	663	3	US-09-693-596-4	Sequence 4, App1	531	65.5	5.5	166	3	US-09-134-001C-4279	Sequence 4279, Ap
459	66.5	5.6	738	3	US-08-867-611-35	Sequence 35, App1	532	65.5	5.5	210	4	US-09-538-092-121	Sequence 121, App
460	66.5	5.6	738	4	US-09-690-359-35	Sequence 35, App1	533	65.5	5.5	291	4	US-09-252-991A-33938	Sequence 32938, A
461	66.5	5.6	738	5	PCT-US92-06965A-5	Sequence 5, App1	534	65.5	5.5	356	4	US-09-107-532A-6286	Sequence 6286, Ap
462	66.5	5.6	750	4	US-09-949-016-7201	Sequence 7201, Ap	535	65.5	5.5	369	3	US-09-172-353-6	Sequence 6, App1
463	66.5	5.6	750	4	US-09-949-016-7202	Sequence 7202, Ap	536	65.5	5.5	369	4	US-09-799-955-6	Sequence 6, App1
464	66.5	5.6	801	4	US-09-710-279-90	Sequence 90, App1	537	65.5	5.5	369	4	US-09-170-496D-26	Sequence 26, App1
465	66.5	5.6	802	3	US-09-134-001C-3741	Sequence 3741, Ap	538	65.5	5.5	369	4	US-09-170-496D-178	Sequence 178, App



539	65.5	5.5	407	4	US-09-252-991A-21511	Sequence 21511, A	612	64.5	5.4	328	4	US-09-489-039A-13216	Sequence 13216, A
540	65.5	5.5	459	4	US-09-694-519-4	Sequence 4	613	64.5	5.4	333	4	US-09-107-532A-4886	Sequence 4886, Ap
541	65.5	5.5	458	4	US-09-252-991A-17314	Sequence 17314, A	614	64.5	5.4	344	2	US-08-726-575A-2	Sequence 2, Appl1
542	65.5	5.5	467	4	US-09-583-110-4658	Sequence 4658, Ap	615	64.5	5.4	349	3	US-09-134-001C-4519	Sequence 4519, Ap
543	65.5	5.5	490	4	US-09-107-433-6940	Sequence 4640, Ap	616	64.5	5.4	393	4	US-09-270-767-42317	Sequence 42317, A
544	65.5	5.5	422	4	US-09-107-532A-6945	Sequence 6945, Ap	617	64.5	5.4	394	4	US-09-107-433-3892	Sequence 3892, Ap
545	65.5	5.5	556	4	US-09-248-796A-15726	Sequence 15726, A	618	64.5	5.4	398	4	US-09-583-110-4666	Sequence 4666, Ap
546	65.5	5.5	630	3	US-09-342-647-2	Sequence 2, Appl1	619	64.5	5.4	400	4	US-09-826-509-491	Sequence 491, App
547	65.5	5.5	718	4	US-09-657-960-3	Sequence 3, Appl1	620	64.5	5.4	407	4	US-09-328-352-5605	Sequence 5605, Ap
548	65.5	5.5	860	1	US-08-032-817-4	Sequence 4, Appl1	621	64.5	5.4	411	2	US-08-336-031-2	Sequence 2, Appl1
549	65.5	5.5	860	3	US-08-485-128-4	Sequence 4, Appl1	622	64.5	5.4	411	2	US-08-902-853-7	Sequence 7, Appl1
550	65.5	5.5	860	4	US-09-804-778A-8	Sequence 8, Appl1	623	64.5	5.4	411	5	PCT-US95-06725-2	Sequence 2, Appl1
551	65.5	5.5	860	4	US-09-824-637-4	Sequence 4, Appl1	624	64.5	5.4	413	4	US-09-799-978-32	Sequence 32, Appl1
552	65.5	5.5	959	4	US-09-248-796A-20776	Sequence 20776, A	625	64.5	5.4	418	5	PCT-US94-03321-72	Sequence 72, Appl1
553	65.5	5.5	1226	2	US-08-540-804-12	Sequence 12, Appl1	626	64.5	5.4	437	3	US-09-353-3321-2	Sequence 2, Appl1
554	65.5	5.5	1226	2	US-08-218-265-12	Sequence 12, Appl1	627	64.5	5.4	437	1	US-07-781-254A-2	Sequence 2, Appl1
555	65.5	5.5	1226	3	US-08-521-872-12	Sequence 12, Appl1	628	64.5	5.4	446	1	US-07-781-254A-3	Sequence 3, Appl1
556	65.5	5.5	1226	3	US-08-590-399-12	Sequence 12, Appl1	629	64.5	5.4	447	4	US-09-252-991A-20563	Sequence 20563, A
557	65.5	5.5	1410	2	US-08-470-058-4	Sequence 4, Appl1	630	64.5	5.4	448	2	US-08-811-897A-18	Sequence 18, Appl1
558	65.5	5.5	1410	3	US-09-037-188-4	Sequence 4, Appl1	631	64.5	5.4	448	2	US-08-855-213-18	Sequence 18, Appl1
559	65.5	5.5	1410	3	US-09-285-310-4	Sequence 4, Appl1	632	64.5	5.4	448	3	US-09-201-474-18	Sequence 18, Appl1
560	65.5	5.5	1410	3	US-09-107-532A-3813	Sequence 3813, Ap	633	64.5	5.4	444	4	US-09-107-532A-5509	Sequence 5509, Ap
561	65.5	5.4	181	3	US-09-126-640-10	Sequence 10, Appl1	634	64.5	5.4	467	2	US-08-811-897A-19	Sequence 19, Appl1
562	65.5	5.4	181	3	US-09-288-292A-10	Sequence 10, Appl1	635	64.5	5.4	467	2	US-08-855-213-19	Sequence 19, Appl1
563	65.5	5.4	182	3	US-08-826-246-8	Sequence 8, Appl1	636	64.5	5.4	467	3	US-09-201-474-19	Sequence 19, Appl1
564	65.5	5.4	182	3	US-08-944-495-8	Sequence 8, Appl1	637	64.5	5.4	476	2	US-08-811-897A-20	Sequence 20, Appl1
565	65.5	5.4	182	3	US-08-925-588-8	Sequence 8, Appl1	638	64.5	5.4	476	2	US-08-855-213-20	Sequence 20, Appl1
566	65.5	5.4	182	4	US-09-372-044-8	Sequence 8, Appl1	639	64.5	5.4	476	2	US-09-201-474-20	Sequence 20, Appl1
567	65.5	5.4	182	4	US-08-825-486-8	Sequence 8, Appl1	640	64.5	5.4	482	4	US-09-107-532A-4512	Sequence 4512, Ap
568	65.5	5.4	182	4	US-08-826-248-8	Sequence 8, Appl1	641	64.5	5.4	483	4	US-09-134-000C-4234	Sequence 4234, Ap
569	65.5	5.4	193	4	US-09-328-352-6034	Sequence 6034, Ap	642	64.5	5.4	486	3	US-09-291-922-10	Sequence 10, Appl1
570	65.5	5.4	223	4	US-10-162-012-9	Sequence 9, Appl1	643	64.5	5.4	487	4	US-09-349-016-9649	Sequence 9649, Ap
571	65.5	5.4	272	4	US-09-903-456-79	Sequence 79, Appl1	644	64.5	5.4	484	2	US-09-031-392-5	Sequence 5, Appl1
572	65.5	5.4	272	4	US-09-949-016-8160	Sequence 8160, Ap	645	64.5	5.4	494	4	US-09-299-549-5	Sequence 5, Appl1
573	65.5	5.4	282	4	US-09-107-532A-5538	Sequence 5538, Ap	646	64.5	5.4	494	3	US-09-610-417-5	Sequence 5, Appl1
574	65.5	5.4	311	4	US-09-252-991A-19489	Sequence 19489, A	647	64.5	5.4	495	2	US-08-811-897A-21	Sequence 21, Appl1
575	65.5	5.4	311	4	US-09-538-092-506	Sequence 506, App	648	64.5	5.4	495	2	US-08-855-213-21	Sequence 21, Appl1
576	65.5	5.4	336	3	US-09-095-163-2	Sequence 2, Appl1	649	64.5	5.4	495	3	US-09-201-474-21	Sequence 21, Appl1
577	65.5	5.4	336	3	US-09-485-648-6	Sequence 6, Appl1	650	64.5	5.4	557	4	US-09-521-1958-27	Sequence 27, Appl1
578	65.5	5.4	336	3	US-09-503-565-6	Sequence 6, Appl1	651	64.5	5.4	557	4	US-09-798-743-3	Sequence 3, Appl1
579	65.5	5.4	336	3	US-09-485-649-6	Sequence 6, Appl1	652	64.5	5.4	576	3	US-09-248-796A-19123	Sequence 19123, A
580	65.5	5.4	375	4	US-09-799-978-8	Sequence 8, Appl1	653	64.5	5.4	576	3	US-08-948-564-16	Sequence 16, Appl1
581	65.5	5.4	401	4	US-09-799-978-8	Sequence 8, Appl1	654	64.5	5.4	747	3	US-09-291-922-2	Sequence 2, Appl1
582	65.5	5.4	415	1	US-08-110-386A-2	Sequence 2, Appl1	655	64.5	5.4	757	4	US-09-585-858-24	Sequence 24, Appl1
583	65.5	5.4	415	3	US-08-482-746-2	Sequence 2, Appl1	656	64.5	5.4	757	4	US-10-270-878A-24	Sequence 24, Appl1
584	65.5	5.4	415	4	US-09-580-734-2	Sequence 2, Appl1	657	64.5	5.4	795	4	US-09-107-532A-5429	Sequence 5429, Ap
585	65.5	5.4	415	4	US-08-374-009-2	Sequence 2, Appl1	658	64.5	5.4	2146	4	US-09-949-016-6947	Sequence 6947, Ap
586	65.5	5.4	415	4	US-09-191-724-2	Sequence 2, Appl1	659	64.5	5.4	3033	1	US-07-925-695-8	Sequence 8, Appl1
587	65.5	5.4	415	4	US-09-799-978-2	Sequence 2, Appl1	660	64.5	5.4	106	4	US-09-370-767-56373	Sequence 56373, A
588	65.5	5.4	415	4	US-09-799-978-4	Sequence 4, Appl1	661	64.5	5.4	106	4	US-09-370-767-56373	Sequence 56373, A
589	65.5	5.4	415	4	US-09-799-978-40	Sequence 40, Appl1	662	64.5	5.4	168	4	US-09-543-681A-6129	Sequence 6129, Ap
590	65.5	5.4	415	4	US-09-826-509-483	Sequence 483, Appl1	663	64.5	5.4	184	4	US-09-48-796A-17465	Sequence 17465, A
591	65.5	5.4	422	4	US-09-710-279-780	Sequence 780, App	664	64.5	5.4	216	4	US-09-270-767-46297	Sequence 46297, A
592	65.5	5.4	441	4	US-09-540-236-2016	Sequence 2016, Ap	665	64.5	5.4	284	4	US-09-270-767-37126	Sequence 37126, A
593	65.5	5.4	461	2	US-08-672-814D-2	Sequence 2, Appl1	666	64.5	5.4	284	4	US-09-270-767-52943	Sequence 52943, A
594	65.5	5.4	461	2	US-09-313-696-2	Sequence 2, Appl1	667	64.5	5.4	284	4	US-09-248-796A-14187	Sequence 14187, A
595	65.5	5.4	461	4	US-09-282-218A-2	Sequence 2, Appl1	668	64.5	5.4	226	3	US-09-100-804-12	Sequence 12, Appl1
596	65.5	5.4	463	3	US-08-612-973-46	Sequence 46, Appl1	669	64.5	5.4	335	4	US-09-107-532A-4900	Sequence 4900, Ap
597	65.5	5.4	463	3	US-08-927-597-46	Sequence 46, Appl1	670	64.5	5.4	336	4	US-09-48-796A-17465	Sequence 17465, A
598	65.5	5.4	463	3	US-08-612-973-36	Sequence 36, Appl1	671	64.5	5.4	331	3	US-08-688-988-28	Sequence 28, Appl1
599	65.5	5.4	460	3	US-08-612-973-36	Sequence 36, Appl1	672	64.5	5.4	335	4	US-09-489-039A-15055	Sequence 15055, A
600	65.5	5.4	460	3	US-08-927-597-36	Sequence 36, Appl1	673	64.5	5.4	363	4	US-09-248-796A-19011	Sequence 19011, A
601	65.5	5.4	491	4	US-09-181-339-7	Sequence 7, Appl1	674	64.5	5.4	364	4	US-09-489-039A-12017	Sequence 12017, A
602	65.5	5.4	516	4	US-09-949-016-11229	Sequence 11229, A	675	64.5	5.4	367	4	US-09-134-001C-4082	Sequence 4082, Ap
603	65.5	5.4	637	4	US-09-543-681A-5869	Sequence 5869, Ap	676	64.5	5.4	337	4	US-08-811-897A-12	Sequence 12, Appl1
604	65.5	5.4	692	3	US-08-612-973-48	Sequence 48, Appl1	677	64.5	5.4	411	1	US-08-981-1893A-12	Sequence 18, Appl1
605	65.5	5.4	692	3	US-08-927-597-48	Sequence 48, Appl1	678	64.5	5.4	411	4	US-09-799-978-18	Sequence 18, Appl1
606	65.5	5.4	809	3	US-08-612-973-50	Sequence 50, Appl1	679	64.5	5.4	411	4	US-09-881-401-4	Sequence 4, Appl1
607	65.5	5.4	809	3	US-08-927-597-50	Sequence 50, Appl1	680	64.5	5.4	412	4	US-09-489-039A-8361	Sequence 8361, Ap
608	65.5	5.4	1033	4	US-09-328-352-5138	Sequence 5138, Ap	681	64.5	5.4	413	4	US-09-491-577-72	Sequence 72, Appl1
609	64.5	5.4	215	4	US-09-107-532A-3730	Sequence 3730, Ap	682	64.5	5.4	416	4	US-09-540-236-2393	Sequence 2393, Ap
610	64.5	5.4	263	1	US-08-565-386-9	Sequence 9, Appl1	683	64.5	5.4	420	4	US-09-583-447A-6	Sequence 6, Appl1
611	64.5	5.4	311	4	US-09-328-352-7066	Sequence 7066, Ap	684	64.5	5.4	431	3	US-08-981-1899A-13	Sequence 13, Appl1
					US-09-252-991A-17395	Sequence 17395, A							

685	64	5.4	431	4	US-09-799-978-20	Sequence 20, Appl	758	63.5	5.3	409	4	US-09-326-203A-23	Sequence 23, Appl
686	64	5.4	431	4	US-09-881-401-2	Sequence 2, Appl1	759	63.5	5.3	416	4	US-09-328-352-4330	Sequence 4300, Ap
687	64	5.4	448	4	US-09-252-991A-23910	Sequence 23910, A	760	63.5	5.3	428	4	US-09-799-978-36	Sequence 36, Appl
688	64	5.4	469	4	US-09-328-352-4250	Sequence 4250, Ap	761	63.5	5.3	437	4	US-09-949-016-8094	Sequence 8094, Ap
689	64	5.4	489	2	US-09-062-890-38	Sequence 38, Appl	762	63.5	5.3	446	2	US-08-672-814D-11	Sequence 11, Appl
690	64	5.4	501	4	US-09-902-540-11195	Sequence 11195, A	763	63.5	5.3	446	3	US-09-533-696-11	Sequence 11, Appl
691	64	5.4	503	4	US-09-583-447A-2	Sequence 2, Appl1	764	63.5	5.3	446	4	US-09-282-218A-19	Sequence 19, Appl
692	64	5.4	504	4	US-09-583-447A-4	Sequence 4, Appl1	765	63.5	5.3	458	4	US-09-252-991A-20655	Sequence 20655, A
693	64	5.4	534	4	US-09-710-379-920	Sequence 920, App	766	63.5	5.3	473	4	US-09-489-039A-10432	Sequence 10432, A
694	64	5.4	554	4	US-09-543-681A-4582	Sequence 4582, Ap	767	63.5	5.3	484	1	US-08-194-338-7	Sequence 7, Appl1
695	64	5.4	586	3	US-09-040-725A-1	Sequence 1, Appl1	768	63.5	5.3	518	4	US-09-543-681A-4949	Sequence 4949, Ap
696	64	5.4	686	4	US-09-134-000C-5066	Sequence 5066, Ap	769	63.5	5.3	568	4	US-09-469-200B-10	Sequence 10, Appl
697	64	5.4	757	4	US-09-585-858-23	Sequence 23, Appl	770	63.5	5.3	759	2	US-08-637-759B-89	Sequence 89, Appl
698	64	5.4	757	4	US-10-270-878-23	Sequence 23, Appl	771	63.5	5.3	759	3	US-08-871-355A-89	Sequence 89, Appl
699	64	5.4	967	1	US-08-188-281B-13	Sequence 13, Appl	772	63.5	5.3	759	3	US-09-201-945-89	Sequence 89, Appl
700	64	5.4	967	5	PCT-US94-07280-13	Sequence 13, Appl	773	63.5	5.3	866	3	US-08-651-999A-1	Sequence 1, Appl1
701	64	5.4	967	5	PCT-US95-01087-13	Sequence 13, Appl	774	63.5	5.3	866	3	US-09-385-752-1	Sequence 1, Appl1
702	64	5.4	1116	4	US-09-543-681A-4379	Sequence 4379, Ap	775	63.5	5.3	2000	4	US-09-382-552-2	Sequence 2, Appl1
703	64	5.4	1462	3	US-07-792-600-31	Sequence 31, Appl	776	63	5.3	147	4	US-09-470-767-45186	Sequence 45186, A
704	64	5.4	1462	3	US-09-157-021-31	Sequence 31, Appl	777	63	5.3	177	4	US-09-492-308A-20	Sequence 20, Appl
705	64	5.4	1462	3	US-09-156-842-31	Sequence 31, Appl	778	63	5.3	180	4	US-09-107-532A-5495	Sequence 5495, Ap
706	64	5.4	1462	4	US-09-591-514-31	Sequence 31, Appl	779	63	5.3	197	4	US-09-198-452A-403	Sequence 403, App
707	64	5.4	1648	1	US-08-188-281B-12	Sequence 12, Appl	780	63	5.3	218	4	US-09-134-001C-4489	Sequence 4489, Ap
708	64	5.4	1648	5	PCT-US94-07280-12	Sequence 12, Appl	781	63	5.3	233	3	US-09-134-001C-4813	Sequence 4013, Ap
709	64	5.4	1648	5	PCT-US95-01087-12	Sequence 12, Appl	782	63	5.3	240	4	US-09-452-991A-29766	Sequence 29766, A
710	64	5.4	2436	3	US-08-444-818-75	Sequence 75, Appl	783	63	5.3	245	4	US-09-949-016-11068	Sequence 11068, A
711	64	5.4	2722	3	US-08-444-818-89	Sequence 89, Appl	784	63	5.3	259	3	US-09-261-599B-3	Sequence 3, Appl1
712	64	5.4	3011	1	US-08-188-281B-1	Sequence 1, Appl1	785	63	5.3	259	4	US-09-456-455A-3	Sequence 3, Appl1
713	64	5.4	3011	1	US-08-453-552-1	Sequence 1, Appl1	786	63	5.3	264	4	US-09-270-767-41787	Sequence 41787, A
714	64	5.4	3011	2	US-08-710-637-1	Sequence 1, Appl1	787	63	5.3	295	4	US-09-583-110-4171	Sequence 4171, Ap
715	64	5.4	3011	5	PCT-US93-00907-1	Sequence 1, Appl1	788	63	5.3	299	4	US-09-107-532A-5499	Sequence 5499, Ap
716	64	5.4	3011	5	PCT-US94-07280-1	Sequence 1, Appl1	789	63	5.3	353	3	US-09-134-001C-3246	Sequence 3246, Ap
717	64	5.4	3011	5	PCT-US95-01087-1	Sequence 1, Appl1	790	63	5.3	359	3	US-08-688-988-32	Sequence 32, Appl
718	64	5.4	118	3	US-09-627-376-17	Sequence 17, Appl	791	63	5.3	361	1	US-08-390-162-4	Sequence 4, Appl1
719	63.5	5.3	118	4	US-10-047-676B-17	Sequence 17, Appl	792	63	5.3	361	1	US-08-685-945B-4	Sequence 2, Appl1
720	63.5	5.3	124	4	US-09-270-767-54829	Sequence 34829, A	793	63	5.3	365	1	US-08-390-162-2	Sequence 2, Appl1
721	63.5	5.3	124	4	US-09-270-767-50046	Sequence 50046, A	794	63	5.3	365	1	US-08-685-945B-2	Sequence 2, Appl1
722	63.5	5.3	134	4	US-09-513-999C-6305	Sequence 6305, Ap	795	63	5.3	366	4	US-09-107-433A-5158	Sequence 5158, Ap
723	63.5	5.3	1209	4	US-09-134-000C-3922	Sequence 3922, Ap	796	63	5.3	370	3	US-09-172-353-2	Sequence 2, Appl1
724	63.5	5.3	219	4	US-09-270-767-41489	Sequence 41489, A	797	63	5.3	370	3	US-09-172-353-3	Sequence 3, Appl1
725	63.5	5.3	228	4	US-09-107-433-3974	Sequence 3974, Ap	798	63	5.3	370	4	US-09-799-955-2	Sequence 2, Appl1
726	63.5	5.3	253	4	US-09-602-787A-8	Sequence 8, Appl1	799	63	5.3	370	4	US-09-799-955-3	Sequence 3, Appl1
727	63.5	5.3	264	4	US-09-489-039A-9738	Sequence 9738, Ap	800	63	5.3	383	4	US-09-710-279-2446	Sequence 2426, Ap
728	63.5	5.3	275	1	US-08-118-270-66	Sequence 66, Appl	801	63	5.3	384	3	US-09-134-001C-3437	Sequence 3437, Ap
729	63.5	5.3	275	5	PCT-US93-08528-66	Sequence 66, Appl	802	63	5.3	415	3	US-08-482-746-13	Sequence 13, Appl
730	63.5	5.3	279	3	US-09-134-001C-4667	Sequence 4667, Ap	803	63	5.3	415	4	US-09-580-734-13	Sequence 13, Appl
731	63.5	5.3	280	1	US-08-781-562-4	Sequence 4, Appl1	804	63	5.3	415	4	US-08-374-009-13	Sequence 13, Appl
732	63.5	5.3	308	4	US-09-252-991A-16800	Sequence 16800, A	805	63	5.3	415	4	US-09-191-724-13	Sequence 22, Appl
733	63.5	5.3	342	3	US-09-116-498-4	Sequence 4, Appl1	806	63	5.3	415	4	US-09-199-978-22	Sequence 12, Appl
734	63.5	5.3	342	3	US-09-116-498-6	Sequence 6, Appl1	807	63	5.3	422	3	US-09-625-188-12	Sequence 2, Appl1
735	63.5	5.3	342	4	US-09-852-156-4	Sequence 6, Appl1	808	63	5.3	431	1	US-08-381-433A-2	Sequence 10991, A
736	63.5	5.3	342	4	US-09-852-156-6	Sequence 6, Appl1	809	63	5.3	441	1	US-09-489-039A-10091	Sequence 5, Appl1
737	63.5	5.3	349	4	US-09-252-991A-24644	Sequence 24644, A	810	63	5.3	450	1	US-08-194-338-5	Sequence 8, Appl1
738	63.5	5.3	350	4	US-09-556-002-2	Sequence 2, Appl1	811	63	5.3	450	1	US-08-444-734A-8	Sequence 4207, Ap
739	63.5	5.3	358	4	US-09-270-767-41449	Sequence 41449, A	812	63	5.3	451	3	US-09-134-001C-4420	Sequence 4420, Ap
740	63.5	5.3	358	4	US-09-933-999A-5	Sequence 5, Appl1	813	63	5.3	489	2	US-09-062-890-34	Sequence 36, Appl
741	63.5	5.3	372	1	US-08-202-056-5	Sequence 5, Appl1	814	63	5.3	489	2	US-09-062-890-36	Sequence 2, Appl1
742	63.5	5.3	372	1	US-08-076-093A-6	Sequence 6, Appl1	815	63	5.3	509	2	US-08-890-980-2	Sequence 2, Appl1
743	63.5	5.3	372	1	US-08-701-265-6	Sequence 6, Appl1	816	63	5.3	509	3	US-08-890-979-2	Sequence 2, Appl1
744	63.5	5.3	372	2	US-08-284-586-6	Sequence 6, Appl1	817	63	5.3	509	3	US-09-032-894-2	Sequence 2, Appl1
745	63.5	5.3	372	2	US-08-805-478-6	Sequence 6, Appl1	818	63	5.3	509	3	US-09-031-626-2	Sequence 2, Appl1
746	63.5	5.3	372	2	US-08-802-627A-6	Sequence 6, Appl1	819	63	5.3	509	4	US-09-054-272-59	Sequence 59, Appl
747	63.5	5.3	372	2	US-08-801-238-6	Sequence 6, Appl1	820	63	5.3	640	4	US-09-252-991A-27542	Sequence 27542, A
748	63.5	5.3	372	2	US-08-801-228-6	Sequence 6, Appl1	821	63	5.3	692	4	US-09-540-236-3150	Sequence 3150, Ap
749	63.5	5.3	372	3	US-09-104-296-6	Sequence 6, Appl1	822	63	5.3	729	3	US-09-291-922-29	Sequence 29, Appl
750	63.5	5.3	372	3	US-08-982-493-8	Sequence 8, Appl1	823	63	5.3	795	4	US-09-252-991A-19085	Sequence 19085, A
751	63.5	5.3	372	4	US-09-170-496D-66	Sequence 66, Appl	824	63	5.3	822	4	US-08-684-932A-38	Sequence 38, Appl
752	63.5	5.3	372	4	US-09-170-496D-200	Sequence 200, App	825	63	5.3	822	4	US-09-618-308B-2	Sequence 2, Appl1
753	63.5	5.3	378	4	US-09-949-016-10255	Sequence 10255, A	826	63	5.3	943	2	US-08-469-537A-107	Sequence 107, App
754	63.5	5.3	379	4	US-09-248-796A-14491	Sequence 14491, A	827	63	5.3	1027	4	US-09-902-540-11750	Sequence 11750, A
755	63.5	5.3	397	4	US-09-583-110-2946	Sequence 2946, Ap	828	63	5.3	1802	3	US-09-322-478-18	Sequence 18, Appl
756	63.5	5.3	404	4	US-09-107-433-3744	Sequence 3747, Ap	829	63	5.3	1802	3	US-09-586-106D-18	Sequence 18, Appl
757	63.5	5.3	406	4	US-09-252-991A-26429	Sequence 26429, A	830	62.5	5.2	80	4	US-09-248-796A-26578	Sequence 26578, A

831	62.5	5.2	136	2	US-08-477-451-31	Sequence 31, Appl	904	62	5.2	272	4	US-09-303-456-81	Sequence 81, Appl
832	62.5	5.2	140	4	US-09-270-767-60416	Sequence 40416, A	905	62	5.2	280	4	US-09-302-540-10330	Sequence 10330, A
833	62.5	5.2	140	4	US-09-270-767-55632	Sequence 55632, A	906	62	5.2	283	4	US-09-303-456-88	Sequence 88, Appl
834	62.5	5.2	161	3	US-09-413-814-15	Sequence 15, Appl	907	62	5.2	288	4	US-09-303-456-84	Sequence 84, Appl
835	62.5	5.2	183	4	US-09-107-532A-7197	Sequence 7197, Ap	908	62	5.2	290	3	US-09-134-001C-4893	Sequence 4893, Ap
836	62.5	5.2	191	4	US-09-270-767-50648	Sequence 50648, A	909	62	5.2	292	4	US-09-303-456-82	Sequence 82, Appl
837	62.5	5.2	191	4	US-09-270-767-55864	Sequence 55864, A	910	62	5.2	295	4	US-09-303-456-86	Sequence 86, Appl
838	62.5	5.2	197	4	US-09-486-147-40	Sequence 40, Appl	911	62	5.2	305	4	US-09-270-767-44944	Sequence 44944, A
839	62.5	5.2	200	4	US-09-270-767-36009	Sequence 36009, A	912	62	5.2	317	4	US-09-489-039A-9602	Sequence 9602, Ap
840	62.5	5.2	200	4	US-09-270-767-51226	Sequence 51226, A	913	62	5.2	323	1	US-07-667-276A-7	Sequence 7, Appl
841	62.5	5.2	214	4	US-09-710-279-774	Sequence 714, App	914	62	5.2	326	1	US-09-543-681A-7161	Sequence 7161, Ap
842	62.5	5.2	221	4	US-09-248-796A-15088	Sequence 15088, A	915	62	5.2	331	2	US-08-560-0988A-46	Sequence 46, Appl
843	62.5	5.2	252	4	US-09-270-767-45203	Sequence 45203, A	916	62	5.2	335	1	US-07-759-568-1	Sequence 1, Appl
844	62.5	5.2	261	4	US-09-338-352-6619	Sequence 6619, Ap	917	62	5.2	335	1	US-08-450-393A-8	Sequence 8, Appl
845	62.5	5.2	304	4	US-09-252-991A-22398	Sequence 22398, A	918	62	5.2	335	2	US-08-390-000A-5	Sequence 5, Appl
846	62.5	5.2	304	4	US-09-107-532A-4681	Sequence 4681, Ap	919	62	5.2	335	3	US-08-446-669-8	Sequence 8, Appl
847	62.5	5.2	327	2	US-08-926-724-1	Sequence 1, Appl	920	62	5.2	335	3	US-09-445-583-53	Sequence 53, Appl
848	62.5	5.2	327	2	US-09-949-016-6562	Sequence 6562, Ap	921	62	5.2	335	3	US-09-534-185-53	Sequence 53, Appl
849	62.5	5.2	341	4	US-09-252-991A-30051	Sequence 30051, A	922	62	5.2	335	4	US-09-625-573-8	Sequence 8, Appl
850	62.5	5.2	342	4	US-09-134-000C-5123	Sequence 5123, Ap	923	62	5.2	335	5	PCT-US95-00476-8	Sequence 8, Appl
851	62.5	5.2	343	4	US-09-743-871B-51	Sequence 714, Ap	924	62	5.2	360	1	US-08-202-056-7	Sequence 7, Appl
852	62.5	5.2	343	4	US-09-743-871B-5	Sequence 5, Appl	925	62	5.2	360	1	US-08-597-236-11	Sequence 11, Appl
853	62.5	5.2	345	4	US-09-543-681A-4410	Sequence 4410, Ap	926	62	5.2	360	1	US-08-746-682A-11	Sequence 11, Appl
854	62.5	5.2	349	3	US-09-162-524-3	Sequence 3, Appl	927	62	5.2	360	1	US-09-409-778-4	Sequence 4, Appl
855	62.5	5.2	349	4	US-09-762-661A-2	Sequence 2, Appl	928	62	5.2	361	4	US-09-710-279-184	Sequence 184, Ap
856	62.5	5.2	353	4	US-09-949-016-8077	Sequence 8077, Ap	929	62	5.2	384	4	US-09-491-577-16	Sequence 16, Appl
857	62.5	5.2	383	5	US-09-330-235-8	Sequence 8, Appl	930	62	5.2	383	4	US-09-252-991A-25633	Sequence 25633, A
858	62.5	5.2	383	5	PCT-US94-01321-2	Sequence 2, Appl	931	62	5.2	405	4	US-09-489-039A-7574	Sequence 7574, Ap
859	62.5	5.2	432	4	US-09-489-039A-7223	Sequence 7223, Ap	932	62	5.2	407	4	US-09-949-016-11348	Sequence 11348, A
860	62.5	5.2	434	4	US-09-198-452A-434	Sequence 434, App	933	62	5.2	409	4	US-09-583-110-3749	Sequence 3749, Ap
861	62.5	5.2	439	4	US-09-438-185A-417	Sequence 417, App	934	62	5.2	412	3	US-09-134-001C-3949	Sequence 3949, Ap
862	62.5	5.2	439	4	US-09-489-039A-13336	Sequence 13336, A	935	62	5.2	413	4	US-09-107-433-2887	Sequence 2887, Ap
863	62.5	5.2	441	4	US-09-248-796A-16114	Sequence 16114, A	936	62	5.2	414	4	US-09-198-452A-414	Sequence 414, App
864	62.5	5.2	442	3	US-08-121-446-4	Sequence 4, Appl	937	62	5.2	414	4	US-09-438-185A-336	Sequence 336, App
865	62.5	5.2	442	4	US-09-520-210-10	Sequence 10, Appl	938	62	5.2	415	4	US-09-799-978-28	Sequence 28, Appl
866	62.5	5.2	442	4	US-09-826-509-497	Sequence 497, App	939	62	5.2	417	4	US-09-710-279-950	Sequence 950, App
867	62.5	5.2	443	3	US-09-161-994A-3	Sequence 3, Appl	940	62	5.2	447	4	US-09-388-089B-2	Sequence 2, Appl
868	62.5	5.2	452	1	US-08-117-361C-1	Sequence 1, Appl	941	62	5.2	473	1	US-08-597-236-13	Sequence 13, Appl
869	62.5	5.2	452	4	US-09-710-279-1834	Sequence 1834, Ap	942	62	5.2	473	1	US-08-746-682A-13	Sequence 13, Appl
870	62.5	5.2	453	4	US-09-489-039A-10468	Sequence 10468, A	943	62	5.2	475	4	US-09-388-089B-12	Sequence 12, Appl
871	62.5	5.2	453	4	US-09-769-863-14	Sequence 14, Appl	944	62	5.2	489	1	US-08-589-893-14	Sequence 14, Appl
872	62.5	5.2	459	4	US-09-489-039A-9027	Sequence 9027, Ap	945	62	5.2	489	1	US-08-589-893-22	Sequence 22, Appl
873	62.5	5.2	463	3	US-09-134-001C-3973	Sequence 3973, Ap	946	62	5.2	489	1	US-08-589-893-24	Sequence 24, Appl
874	62.5	5.2	476	4	US-09-489-039A-13646	Sequence 13646, A	947	62	5.2	489	2	US-09-020-991-14	Sequence 14, Appl
875	62.5	5.2	480	4	US-09-489-039A-13045	Sequence 13045, A	948	62	5.2	489	2	US-09-020-991-22	Sequence 22, Appl
876	62.5	5.2	539	4	US-09-949-016-6363	Sequence 6363, Ap	949	62	5.2	489	2	US-09-020-991-24	Sequence 24, Appl
877	62.5	5.2	541	3	US-09-158-767-19	Sequence 19, Appl	950	62	5.2	489	2	US-09-062-890-14	Sequence 14, Appl
878	62.5	5.2	541	3	US-09-158-767-20	Sequence 20, Appl	951	62	5.2	489	2	US-09-062-890-22	Sequence 22, Appl
879	62.5	5.2	541	4	US-09-713-794-19	Sequence 19, Appl	952	62	5.2	489	2	US-09-062-890-24	Sequence 24, Appl
880	62.5	5.2	557	1	US-09-713-794-20	Sequence 20, Appl	953	62	5.2	488	4	US-09-388-089B-11	Sequence 11, Appl
881	62.5	5.2	578	1	US-08-424-788-6	Sequence 6, Appl	954	62	5.2	489	4	US-09-673-898-6	Sequence 6, Appl
882	62.5	5.2	578	1	US-08-424-788-5	Sequence 5, Appl	955	62	5.2	557	3	US-09-560-639-7	Sequence 7, Appl
883	62.5	5.2	578	1	US-08-110-683-2	Sequence 2, Appl	956	62	5.2	567	3	US-09-173-151A-24	Sequence 24, Appl
884	62.5	5.2	578	2	US-08-683-743-2	Sequence 2, Appl	957	62	5.2	567	3	US-09-032-337-39	Sequence 39, Appl
885	62.5	5.2	578	2	US-08-477-166-2	Sequence 2, Appl	958	62	5.2	582	3	US-08-194-560-2	Sequence 2, Appl
886	62.5	5.2	578	2	US-08-472-097-2	Sequence 2, Appl	959	62	5.2	602	3	US-09-134-001C-4416	Sequence 4416, Ap
887	62.5	5.2	578	4	US-09-439-672-2	Sequence 2, Appl	960	62	5.2	638	3	US-09-376-781-6	Sequence 6, Appl
888	62.5	5.2	578	5	PCT-US93-11638-2	Sequence 2, Appl	961	62	5.2	706	4	US-09-538-092-957	Sequence 957, App
889	62.5	5.2	605	4	US-09-328-352-7890	Sequence 7890, Ap	962	62	5.2	747	4	US-09-949-016-10040	Sequence 10040, A
890	62.5	5.2	628	4	US-09-107-532A-5288	Sequence 5288, Ap	963	62	5.2	775	3	US-09-305-640-2	Sequence 2, Appl
891	62.5	5.2	669	3	US-09-342-647-18	Sequence 18, Appl	964	62	5.2	800	4	US-09-248-796A-20101	Sequence 20101, A
892	62.5	5.2	765	4	US-09-134-000C-6660	Sequence 6660, Ap	965	62	5.2	1186	1	US-08-602-737-6	Sequence 6, Appl
893	62.5	5.2	766	4	US-09-270-767-00617	Sequence 46617, Ap	966	62	5.2	1186	3	US-09-001-982-6	Sequence 6, Appl
894	62.5	5.2	796	4	US-09-270-767-55833	Sequence 55833, A	967	62	5.2	1186	4	US-09-668-650-6	Sequence 6, Appl
895	62.5	5.2	1414	4	US-09-902-540-10957	Sequence 10957, A	968	62	5.2	1267	4	US-09-445-681A-6130	Sequence 6130, Ap
896	62.5	5.2	1768	4	US-09-489-039A-11704	Sequence 11704, A	969	62	5.2	1985	4	US-09-495-714A-6	Sequence 6, Appl
897	62.5	5.2	91	4	US-09-248-796A-23462	Sequence 23462, A	970	61.5	5.1	130	4	US-09-949-016-8171	Sequence 8171, Ap
898	62.5	5.2	112	4	US-09-270-767-59183	Sequence 59183, A	971	61.5	5.1	163	3	US-08-600-430-4	Sequence 4, Appl
899	62.5	5.2	129	4	US-09-673-898-10	Sequence 10, Appl	972	61.5	5.1	170	4	US-09-710-279-1164	Sequence 1164, Ap
900	62.5	5.2	250	4	US-09-270-767-43784	Sequence 43784, A	973	61.5	5.1	186	3	US-09-134-001C-4095	Sequence 4095, Ap
901	62.5	5.2	254	4	US-09-248-796A-22532	Sequence 22532, A	974	61.5	5.1	188	4	US-09-902-540-11995	Sequence 11995, A
902	62.5	5.2	272	4	US-09-903-456-76	Sequence 76, Appl	975	61.5	5.1	235	3	US-08-812-586-16	Sequence 16, Appl
903	62.5	5.2	272	4	US-09-903-456-80	Sequence 80, Appl	976	61.5	5.1	235	4	US-09-535-832A-17	Sequence 17, Appl

977	61.5	5.1	260	4	US-09-540-236-3812	Sequence 3812, Ap	1050	61.5	5.1	2247	4	US-09-660-541-2	Sequence 2, Appl1
978	61.5	5.1	269	4	US-09-489-039A-9180	Sequence 9180, Ap	1051	61.5	5.1	3066	3	US-08-952-127-12	Sequence 12, Appl1
979	61.5	5.1	271	3	US-09-077-675A-12	Sequence 12, Appl	1052	61	5.1	95	4	US-09-248-796A-21665	Sequence 21665, A
980	61.5	5.1	271	4	US-09-077-674-12	Sequence 127, Appl	1053	61	5.1	122	4	US-09-710-279-102	Sequence 102, App
981	61.5	5.1	288	4	US-09-134-000C-5520	Sequence 5520, Ap	1054	61	5.1	175	2	US-08-408-095-11	Sequence 11, Appl
982	61.5	5.1	289	4	US-09-489-039A-12390	Sequence 12390, A	1055	61	5.1	188	4	US-09-198-452A-1206	Sequence 1206, Ap
983	61.5	5.1	297	4	US-09-328-352-5769	Sequence 5769, Ap	1056	61	5.1	199	3	US-09-080-643-4	Sequence 4, Appl1
984	61.5	5.1	302	3	US-09-077-675A-2	Sequence 2, Appl1	1057	61	5.1	200	4	US-09-710-279-394	Sequence 394, Appl
985	61.5	5.1	302	3	US-09-077-675A-7	Sequence 7, Appl1	1058	61	5.1	200	4	US-09-710-279-1242	Sequence 1242, Ap
986	61.5	5.1	302	4	US-09-077-674-2	Sequence 2, Appl1	1059	61	5.1	202	4	US-08-657-749D-17	Sequence 17, Appl
987	61.5	5.1	302	4	US-09-077-674-7	Sequence 7, Appl1	1060	61	5.1	206	3	US-09-134-001C-3929	Sequence 3929, Ap
988	61.5	5.1	343	4	US-09-543-681A-6853	Sequence 6853, Ap	1061	61	5.1	207	3	US-08-559-397A-13	Sequence 13, Appl1
989	61.5	5.1	349	4	US-09-270-767-38347	Sequence 38347, A	1062	61	5.1	209	3	US-08-559-397A-11	Sequence 11, Appl
990	61.5	5.1	349	4	US-09-270-767-53564	Sequence 53564, A	1063	61	5.1	225	4	US-09-252-991A-30213	Sequence 30213, A
991	61.5	5.1	353	3	US-09-077-675A-3	Sequence 3, Appl1	1064	61	5.1	220	3	US-09-134-001C-3744	Sequence 3744, Ap
992	61.5	5.1	353	4	US-09-077-674-3	Sequence 3, Appl1	1065	61	5.1	239	4	US-09-710-279-978	Sequence 978, App
993	61.5	5.1	361	3	US-09-077-675A-8	Sequence 8, Appl1	1066	61	5.1	241	4	US-09-489-039A-8397	Sequence 8397, Ap
994	61.5	5.1	361	4	US-09-077-674-8	Sequence 8, Appl1	1067	61	5.1	266	1	US-08-236-918A-6	Sequence 6, Appl1
995	61.5	5.1	366	3	US-09-077-675A-13	Sequence 13, Appl	1068	61	5.1	266	3	US-09-150-864A-6	Sequence 6, Appl1
996	61.5	5.1	366	4	US-09-077-674-13	Sequence 13, Appl	1069	61	5.1	266	4	US-08-012-269A-2	Sequence 2, Appl1
997	61.5	5.1	366	4	US-09-170-496D-88	Sequence 88, Appl	1070	61	5.1	266	4	US-09-623-545A-3	Sequence 3, Appl1
998	61.5	5.1	366	4	US-09-743-742B-7	Sequence 7, Appl1	1071	61	5.1	266	5	PCT-US96-03965-2	Sequence 2, Appl1
999	61.5	5.1	366	4	US-09-762-661A-5	Sequence 5, Appl1	1072	61	5.1	261	3	US-09-134-001C-3485	Sequence 3485, Ap
1000	61.5	5.1	366	4	US-09-762-661A-5	Sequence 5, Appl1	1073	61	5.1	265	4	US-09-107-532A-6716	Sequence 6716, Ap
1001	61.5	5.1	366	4	US-09-364-425B-45	Sequence 45, Appl1	1074	61	5.1	272	4	US-09-903-456-78	Sequence 78, Appl
1002	61.5	5.1	366	4	US-09-743-475-4	Sequence 4, Appl1	1075	61	5.1	277	4	US-09-583-110-3171	Sequence 3171, Ap
1003	61.5	5.1	366	4	US-09-743-475-6	Sequence 6, Appl1	1076	61	5.1	279	4	US-09-107-433-3691	Sequence 3691, Ap
1004	61.5	5.1	376	2	US-08-465-976A-3	Sequence 3, Appl1	1077	61	5.1	281	4	US-10-121-857-45	Sequence 45, Appl1
1005	61.5	5.1	376	2	US-08-982-412-3	Sequence 3, Appl1	1078	61	5.1	285	4	US-09-543-681A-7666	Sequence 7666, Ap
1006	61.5	5.1	376	4	US-09-107-433-3823	Sequence 3823, Ap	1079	61	5.1	266	4	US-09-540-236-2583	Sequence 2583, Ap
1007	61.5	5.1	379	3	US-09-740-035-4	Sequence 4, Appl1	1080	61	5.1	288	4	US-09-438-185A-545	Sequence 545, App
1008	61.5	5.1	391	1	US-07-921-178A-2	Sequence 2, Appl1	1081	61	5.1	302	4	US-08-311-731A-173	Sequence 173, App
1009	61.5	5.1	391	1	US-08-103-445-5	Sequence 5, Appl1	1082	61	5.1	338	4	US-09-107-532A-6222	Sequence 6222, Ap
1010	61.5	5.1	391	2	US-08-461-690B-5	Sequence 5, Appl1	1083	61	5.1	345	4	US-09-107-532A-5817	Sequence 5817, Ap
1011	61.5	5.1	391	2	US-08-501-003A-16	Sequence 16, Appl	1084	61	5.1	345	4	US-09-489-039A-7417	Sequence 7417, Ap
1012	61.5	5.1	392	4	US-09-275-252A-13	Sequence 13, Appl	1085	61	5.1	355	4	US-08-833-752-8	Sequence 8, Appl1
1013	61.5	5.1	392	4	US-09-489-039A-8713	Sequence 8713, Ap	1086	61	5.1	355	4	US-09-938-719-8	Sequence 8, Appl1
1014	61.5	5.1	411	2	US-08-741-134-6	Sequence 6, Appl1	1087	61	5.1	358	4	US-09-939-2266-8	Sequence 8, Appl1
1015	61.5	5.1	411	2	US-08-981-189B-10	Sequence 10, Appl	1088	61	5.1	383	4	US-09-248-796A-19081	Sequence 19081, A
1016	61.5	5.1	415	3	US-08-110-286A-6	Sequence 6, Appl1	1089	61	5.1	353	3	US-08-688-988-30	Sequence 30, Appl
1017	61.5	5.1	415	3	US-08-981-189B-10	Sequence 10, Appl	1090	61	5.1	408	4	US-09-328-352-5768	Sequence 5768, Ap
1018	61.5	5.1	415	3	US-08-482-746-6	Sequence 6, Appl1	1091	61	5.1	440	4	US-09-489-039A-12132	Sequence 12132, A
1019	61.5	5.1	415	4	US-09-580-734-6	Sequence 6, Appl1	1092	61	5.1	445	4	US-09-799-978-34	Sequence 34, Appl
1020	61.5	5.1	415	4	US-08-374-009-6	Sequence 6, Appl1	1093	61	5.1	481	4	US-09-248-796A-16683	Sequence 16683, A
1021	61.5	5.1	415	4	US-09-191-724-6	Sequence 6, Appl1	1094	61	5.1	488	4	US-09-489-039A-15101	Sequence 15101, A
1022	61.5	5.1	415	4	US-09-799-978-16	Sequence 16, Appl	1095	61	5.1	489	4	US-09-710-279-2632	Sequence 2632, Ap
1023	61.5	5.1	417	4	US-09-252-991A-26638	Sequence 26638, A	1096	61	5.1	500	4	US-09-134-000C-4886	Sequence 4886, Ap
1024	61.5	5.1	418	4	US-09-543-681A-7634	Sequence 7634, Ap	1097	61	5.1	533	3	US-09-134-001C-3948	Sequence 3948, Ap
1025	61.5	5.1	427	4	US-09-942-501-2	Sequence 2, Appl1	1098	61	5.1	545	4	US-09-949-016-6459	Sequence 6459, Ap
1026	61.5	5.1	458	4	US-09-252-991A-28897	Sequence 28897, A	1099	61	5.1	558	4	US-09-949-016-7736	Sequence 7736, Ap
1027	61.5	5.1	469	4	US-08-956-171B-5245	Sequence 5245, Ap	1100	61	5.1	672	4	US-09-556-916-26	Sequence 26, Appl
1028	61.5	5.1	469	4	US-08-781-986A-5245	Sequence 5245, Ap	1101	61	5.1	672	4	US-09-556-916-28	Sequence 28, Appl
1029	61.5	5.1	479	2	US-08-889-514-2	Sequence 2, Appl1	1102	61	5.1	724	4	US-09-252-991A-30228	Sequence 30228, A
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1031	61.5	5.1	497	1	US-08-633-485-6	Sequence 6, Appl1	1104	61	5.1	737	4	US-09-248-796A-14319	Sequence 14319, A
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1034	61.5	5.1	526	1	US-08-298-426-4	Sequence 4, Appl1	1107	61	5.1	815	4	US-09-107-433-5059	Sequence 5059, Ap
1035	61.5	5.1	615	4	US-09-602-787A-534	Sequence 534, App	1108	61	5.1	848	4	US-09-583-110-2738	Sequence 2738, Ap
1036	61.5	5.1	615	4	US-09-602-787A-536	Sequence 536, App	1109	61	5.1	880	4	US-09-538-092-577	Sequence 577, App
1037	61.5	5.1	659	4	US-09-583-110-5110	Sequence 5110, App	1110	61	5.1	915	4	US-09-107-532A-37114	Sequence 3714, App
1038	61.5	5.1	674	4	US-09-538-092-1125	Sequence 1125, Ap	1111	61	5.1	1088	4	US-09-949-016-8011	Sequence 8011, Ap
1039	61.5	5.1	685	4	US-09-720-317A-31	Sequence 31, Appl	1112	61	5.1	1129	4	US-09-252-991A-31121	Sequence 31121, A
1040	61.5	5.1	692	4	US-09-248-796A-18612	Sequence 18612, A	1113	61	5.1	1336	4	US-09-949-016-9879	Sequence 9879, Ap
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1042	61.5	5.1	817	1	US-08-381-931B-2	Sequence 2, Appl1	1115	61	5.1	1503	4	US-09-949-016-6341	Sequence 6341, Ap
1043	61.5	5.1	865	4	US-09-902-540-10416	Sequence 10416, A	1116	61	5.1	1579	4	US-09-949-016-11100	Sequence 11100, A
1044	61.5	5.1	895	4	US-09-489-039A-13127	Sequence 13127, A	1117	61	5.1	1579	4	US-09-949-016-8301	Sequence 8301, Ap
1045	61.5	5.1	965	4	US-09-437-277-3	Sequence 3, Appl1	1118	61	5.1	2864	4	US-08-469-260A-394	Sequence 394, App
1046	61.5	5.1	1025	4	US-09-543-681A-7112	Sequence 7112, Ap	1119	61	5.1	2864	4	US-08-488-446-394	Sequence 394, App
1047	61.5	5.1	2232	3	US-09-091-219-25	Sequence 25, Appl	1120	61	5.1	2864	4	US-08-467-344A-334	Sequence 334, App
1048	61.5	5.1	2232	3	US-09-660-541-25	Sequence 25, Appl	1121	61	5.1	3011	4	US-08-424-550D-394	Sequence 394, App
1049	61.5	5.1	2247	3	US-09-091-219-2	Sequence 2, Appl1	1122	61	5.1	3011	3	US-08-811-566-20	Sequence 20, Appl

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1124	61	5.1	3011	3	US-09-034-756-20	Sequence 20, Appl1	1197	60.5	5.1	537	3	US-09-134-001C-4091	Sequence 4091, Ap
1125	61	5.1	3011	4	US-10-104-966-1	Sequence 1, Appl1	1198	60.5	5.1	534	3	US-09-134-001C-5109	Sequence 5109, Ap
1126	61	5.1	3011	4	US-09-952-572-9	Sequence 9, Appl1	1199	60.5	5.1	554	4	US-09-543-681A-5774	Sequence 5774, Ap
1127	61	5.1	3012	3	US-08-811-566-2	Sequence 2, Appl1	1200	60.5	5.1	558	4	US-09-540-236-2943	Sequence 2943, Ap
1128	61	5.1	3012	3	US-09-034-756-2	Sequence 2, Appl1	1201	60.5	5.1	665	4	US-09-595-684B-35	Sequence 35, Appl1
1129	60.5	5.1	73	4	US-09-543-681A-6595	Sequence 6595, Ap	1202	60.5	5.1	682	4	US-09-107-532A-4499	Sequence 4499, Ap
1130	60.5	5.1	107	4	US-09-107-532A-5805	Sequence 5805, Ap	1203	60.5	5.1	694	4	US-09-248-796A-20210	Sequence 20210, A
1131	60.5	5.1	116	4	US-09-270-767-36280	Sequence 36280, A	1204	60.5	5.1	726	4	US-09-107-532A-6007	Sequence 6007, Ap
1132	60.5	5.1	116	4	US-09-270-767-51497	Sequence 51497, A	1205	60.5	5.1	865	4	US-09-612-204A-24	Sequence 24, Appl1
1133	60.5	5.1	157	4	US-09-270-767-32124	Sequence 32124, A	1206	60.5	5.1	1064	4	US-09-248-796A-16640	Sequence 16640, A
1134	60.5	5.1	157	4	US-09-270-767-47341	Sequence 47341, A	1207	60.5	5.1	1225	4	US-09-949-016-9468	Sequence 9468, Ap
1135	60.5	5.1	157	4	US-09-270-767-58298	Sequence 58298, A	1208	60.5	5.1	1333	4	US-09-270-767-46728	Sequence 46728, A
1136	60.5	5.1	159	6	5208144-4-32	Patent No. 5208144	1209	60.5	5.1	1912	3	US-08-913-832A-2	Sequence 2, Appl1
1137	60.5	5.1	159	6	5208144-4-32	Patent No. 5208144	1210	60.5	5.1	1912	3	US-08-913-832A-2	Sequence 2, Appl1
1138	60.5	5.1	159	6	5208144-4-32	Patent No. 5208144	1211	60.5	5.1	1912	3	US-08-913-832A-2	Sequence 2, Appl1
1139	60.5	5.1	194	4	US-09-270-767-34926	Sequence 34926, A	1212	60.5	5.1	5032	4	US-09-338-092-979	Sequence 979, Ap
1140	60.5	5.1	195	4	US-09-612-204B-2	Sequence 2, Appl1	1213	60	5.0	136	4	US-09-270-767-31761	Sequence 31761, A
1141	60.5	5.1	197	4	US-09-612-204B-2	Sequence 2, Appl1	1214	60	5.0	136	4	US-09-270-767-46978	Sequence 46978, A
1142	60.5	5.1	198	4	US-09-976-451-5	Sequence 5, Appl1	1215	60	5.0	162	4	US-09-134-000C-4993	Sequence 4993, Ap
1143	60.5	5.1	199	3	US-08-478-316-33	Sequence 33, Appl1	1216	60	5.0	177	4	US-09-492-308A-23	Sequence 23, Appl1
1144	60.5	5.1	199	3	US-09-019-793A-33	Sequence 33, Appl1	1217	60	5.0	189	3	US-09-080-643-2	Sequence 2, Appl1
1145	60.5	5.1	200	2	US-08-799-464A-9	Sequence 9, Appl1	1218	60	5.0	189	4	US-09-270-767-32341	Sequence 32341, A
1146	60.5	5.1	200	4	US-09-601-326-33	Sequence 33, Appl1	1219	60	5.0	189	4	US-09-270-767-47558	Sequence 47558, A
1147	60.5	5.1	200	5	PCT-US95-03927-9	Sequence 9, Appl1	1220	60	5.0	191	4	US-09-583-110-3197	Sequence 3197, Ap
1148	60.5	5.1	207	4	US-08-811-519-18	Sequence 18, Appl1	1221	60	5.0	199	4	US-09-107-433-3384	Sequence 3384, Ap
1149	60.5	5.1	222	4	US-09-270-767-42973	Sequence 42973, A	1222	60	5.0	204	4	US-09-110-279-3240	Sequence 3240, Ap
1150	60.5	5.1	240	2	US-08-114-555A-6	Sequence 6, Appl1	1223	60	5.0	206	3	US-08-513-974B-27	Sequence 27, Appl1
1151	60.5	5.1	240	3	US-08-559-397A-12	Sequence 12, Appl1	1224	60	5.0	206	3	US-08-513-974B-27	Sequence 27, Appl1
1152	60.5	5.1	259	4	US-09-248-796A-22276	Sequence 22276, A	1225	60	5.0	206	4	US-09-461-436B-27	Sequence 27, Appl1
1153	60.5	5.1	280	3	US-08-652-877-6	Sequence 6, Appl1	1226	60	5.0	206	4	US-09-576-290-102	Sequence 22, Appl1
1154	60.5	5.1	280	3	US-08-476-515A-6	Sequence 6, Appl1	1227	60	5.0	214	4	US-09-489-039A-11059	Sequence 11059, A
1155	60.5	5.1	283	1	US-08-118-370-78	Sequence 78, Appl1	1228	60	5.0	223	3	US-08-513-974B-315	Sequence 315, App
1156	60.5	5.1	283	5	PCT-US93-08528-78	Sequence 78, Appl1	1229	60	5.0	223	3	US-08-513-974B-315	Sequence 315, App
1157	60.5	5.1	285	4	US-10-162-012-37	Sequence 37, Appl1	1230	60	5.0	223	3	US-08-513-974B-315	Sequence 315, App
1158	60.5	5.1	296	4	US-09-540-236-2856	Sequence 2856, Ap	1231	60	5.0	223	3	US-08-776-971-100	Sequence 100, App
1159	60.5	5.1	300	4	US-09-393-634-17	Sequence 17, Appl1	1232	60	5.0	223	3	US-08-776-971-100	Sequence 100, App
1160	60.5	5.1	342	2	US-08-742-011-2	Sequence 2, Appl1	1233	60	5.0	223	3	US-08-776-971-100	Sequence 100, App
1161	60.5	5.1	342	3	US-09-275-384B-5	Sequence 5, Appl1	1234	60	5.0	223	4	US-09-576-290-100	Sequence 100, App
1162	60.5	5.1	342	3	US-09-116-498-2	Sequence 2, Appl1	1235	60	5.0	223	4	US-09-576-290-100	Sequence 102, App
1163	60.5	5.1	342	3	US-09-449-437A-2	Sequence 9, Appl1	1236	60	5.0	223	4	US-09-576-290-100	Sequence 108, App
1164	60.5	5.1	342	3	US-09-517-605-9	Sequence 9, Appl1	1237	60	5.0	242	3	US-08-908-332-2	Sequence 2, Appl1
1165	60.5	5.1	342	4	US-09-852-156-2	Sequence 2, Appl1	1238	60	5.0	257	4	US-09-543-681A-6362	Sequence 6362, Ap
1166	60.5	5.1	342	4	US-09-721-341-9	Sequence 9, Appl1	1239	60	5.0	273	4	US-09-248-796A-14625	Sequence 14625, A
1167	60.5	5.1	342	4	US-09-721-495B-9	Sequence 9, Appl1	1240	60	5.0	282	4	US-09-270-767-35685	Sequence 35685, A
1168	60.5	5.1	349	4	US-09-710-879-932	Sequence 932, App	1241	60	5.0	282	4	US-09-270-767-35685	Sequence 35685, A
1169	60.5	5.1	352	4	US-09-489-039A-9155	Sequence 9155, Ap	1242	60	5.0	284	4	US-09-270-767-50902	Sequence 50902, A
1170	60.5	5.1	357	4	US-09-107-532A-5132	Sequence 5132, Ap	1243	60	5.0	295	3	US-09-522-991A-26771	Sequence 10, Appl1
1171	60.5	5.1	359	2	US-08-748-485-5	Sequence 5, Appl1	1244	60	5.0	295	3	US-09-422-968-10	Sequence 10, Appl1
1172	60.5	5.1	388	4	US-09-252-991A-22979	Sequence 22979, A	1245	60	5.0	295	4	US-09-708-015A-10	Sequence 10, Appl1
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1174	60.5	5.1	409	2	US-08-743-130A-2	Sequence 2, Appl1	1247	60	5.0	317	3	US-08-505-284B-17	Sequence 17, Appl1
1175	60.5	5.1	409	2	US-08-743-130A-39	Sequence 39, Appl1	1248	60	5.0	324	4	US-09-543-681A-6241	Sequence 6241, Ap
1176	60.5	5.1	417	4	US-09-248-796A-16410	Sequence 16410, A	1249	60	5.0	326	4	US-09-540-236-3340	Sequence 3340, Ap
1177	60.5	5.1	444	3	US-09-161-994A-4	Sequence 4, Appl1	1250	60	5.0	328	4	US-09-543-681A-5522	Sequence 5252, Ap
1178	60.5	5.1	446	4	US-09-489-039A-9587	Sequence 9587, Ap	1251	60	5.0	330	4	US-09-543-681A-7116	Sequence 7116, Ap
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1180	60.5	5.1	473	4	US-09-489-039A-14199	Sequence 14199, A	1253	60	5.0	333	4	US-09-170-4960-168	Sequence 168, App
1181	60.5	5.1	475	4	US-09-270-767-43475	Sequence 43475, A	1254	60	5.0	333	4	US-09-826-509-509	Sequence 509, App
1182	60.5	5.1	487	3	US-09-724-224-8	Sequence 8, Appl1	1255	60	5.0	341	4	US-09-902-540-11473	Sequence 11473, A
1183	60.5	5.1	487	3	US-10-093-317-8	Sequence 8, Appl1	1256	60	5.0	347	4	US-09-107-532A-6019	Sequence 6019, Ap
1184	60.5	5.1	489	4	US-09-986-536-2	Sequence 2, Appl1	1257	60	5.0	359	4	US-09-107-532A-6455	Sequence 6455, Ap
1185	60.5	5.1	490	4	US-09-248-796A-19910	Sequence 19910, A	1258	60	5.0	360	4	US-09-270-767-32827	Sequence 32827, A
1186	60.5	5.1	490	4	US-09-949-016-8784	Sequence 8784, Ap	1259	60	5.0	360	4	US-09-270-767-48044	Sequence 48044, A
1187	60.5	5.1	498	4	US-09-107-532A-5082	Sequence 5082, Ap	1260	60	5.0	376	4	US-09-107-532A-6648	Sequence 6448, Ap
1188	60.5	5.1	498	4	US-09-583-110-2949	Sequence 2949, Ap	1261	60	5.0	377	3	US-09-316-080-5	Sequence 5, Appl1
1189	60.5	5.1	499	4	US-09-710-879-1558	Sequence 1558, Ap	1262	60	5.0	382	2	US-09-134-001C-4483	Sequence 4483, Ap
1190	60.5	5.1	503	3	US-09-068-195-24	Sequence 24, Appl1	1263	60	5.0	387	2	US-08-902-853-6	Sequence 6, Appl1
1191	60.5	5.1	510	4	US-09-107-433-2618	Sequence 2618, Ap	1264	60	5.0	397	2	US-08-990-379-8	Sequence 8, Appl1
1192	60.5	5.1	512	3	US-09-724-224-4	Sequence 4, Appl1	1265	60	5.0	416	4	US-09-583-110-2732	Sequence 2732, Ap
1193	60.5	5.1	512	4	US-10-093-317-4	Sequence 4, Appl1	1266	60	5.0	416	4	US-10-140-372-4	Sequence 4, Appl1
1194	60.5	5.1	519	4	US-09-248-796A-20852	Sequence 20852, A	1267	60	5.0	418	4	US-09-107-433-3218	Sequence 3218, Ap
1195	60.5	5.1	533	4	US-09-489-039A-7452	Sequence 7452, Ap	1268	60	5.0	419	1	US-08-385-186-2	Sequence 2, Appl1

1269	60	5.0	419	1	US-08-385-186-4	Sequence 4, Appl1	1342	59.5	5.0	209	4	US-09-813-4538-21	Sequence 21, Appl1
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1271	60	5.0	419	4	US-09-949-016-6002	Sequence 6002, Ap	1344	59.5	5.0	222	4	US-09-107-5328-6747	Sequence 6747, Ap
1272	60	5.0	430	4	US-09-799-978-42	Sequence 42, Appl1	1345	59.5	5.0	229	4	US-09-328-352-4690	Sequence 4690, Ap
1273	60	5.0	421	4	US-09-543-681A-7791	Sequence 7791, Ap	1346	59.5	5.0	248	4	US-09-902-540-14104	Sequence 14104, A
1274	60	5.0	422	4	US-09-540-236-2283	Sequence 2283, Ap	1347	59.5	5.0	275	4	US-09-371-056-10	Sequence 10, Appl1
1275	60	5.0	448	4	US-09-949-016-10558	Sequence 10558, A	1348	59.5	5.0	280	4	US-09-543-681A-6175	Sequence 6175, Ap
1276	60	5.0	448	3	US-09-134-001C-4146	Sequence 4146, Ap	1349	59.5	5.0	281	4	US-09-134-000C-4344	Sequence 4344, Ap
1277	60	5.0	467	3	US-08-867-611-28	Sequence 28, Appl1	1350	59.5	5.0	283	4	US-09-107-5328-4206	Sequence 4206, Ap
1278	60	5.0	467	3	US-08-690-359-28	Sequence 33, Appl1	1351	59.5	5.0	295	4	US-09-543-681A-5660	Sequence 5660, Ap
1279	60	5.0	467	5	PCT-US97-06965A-33	Sequence 33, Appl1	1352	59.5	5.0	324	4	US-09-902-540-12246	Sequence 12246, A
1280	60	5.0	502	1	US-08-484-840-3	Sequence 3, Appl1	1353	59.5	5.0	327	2	US-08-926-724-3	Sequence 3, Appl1
1281	60	5.0	502	1	US-08-483-094-3	Sequence 3, Appl1	1354	59.5	5.0	327	3	US-08-904-032-3	Sequence 3, Appl1
1282	60	5.0	509	4	US-09-134-000C-5949	Sequence 5949, Ap	1355	59.5	5.0	337	4	US-09-540-236-2590	Sequence 2590, Ap
1283	60	5.0	521	4	US-09-538-092-1330	Sequence 1330, Ap	1356	59.5	5.0	341	1	US-08-423-564-5	Sequence 5, Appl1
1284	60	5.0	521	4	US-09-949-016-6672	Sequence 6672, Ap	1357	59.5	5.0	350	1	US-08-118-270-41	Sequence 41, Appl1
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1292	60	5.0	626	1	US-07-938-782A-2	Sequence 2, Appl1	1365	59.5	5.0	431	2	US-08-933-750C-24	Sequence 24, Appl1
1293	60	5.0	626	1	US-08-630-524-2	Sequence 2, Appl1	1366	59.5	5.0	431	3	US-09-234-613-24	Sequence 24, Appl1
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1296	60	5.0	630	4	US-09-602-787A-548	Sequence 548, Ap	1369	59.5	5.0	445	4	US-09-710-279-2644	Sequence 2644, Ap
1297	60	5.0	639	3	US-09-134-001C-5661	Sequence 5661, Ap	1370	59.5	5.0	447	4	US-09-694-519-9	Sequence 9, Appl1
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1488	59	4.9	714	2	US-08-990-114-3	Sequence 3, Appl
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## ALIGNMENTS

RESULT 1  
US-08-691-814B-6  
Sequence 6, Application US/08691814B  
Patent No. 5981218  
GENERAL INFORMATION:  
APPLICANT: Rio, Marie-Christine  
APPLICANT: Tomasetto, Catherine  
APPLICANT: Bassett, Paul  
APPLICANT: Byrne, Jennifer  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful  
TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kesseler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Ave, NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/691,814B  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/002,183  
FILING DATE: 09-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1383, 0090001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-691-814B-6

Query Match 55.6%; Score 664; DB 2; Length 445;  
Best Local Similarity 56.2%; Pred. No. 7.5e-68;  
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

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RESULT 2
US-09-949-016-8594
; Sequence 8594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8594
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8594

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RESULT 3
US-08-846-762-92
: Sequence 92, Application US/08846762A
: Patent No. 5994072
: GENERAL INFORMATION:
: APPLICANT: Lam, Joseph S.
: APPLICANT: Burrows, Lori
: APPLICANT: Charter, Deborah
: APPLICANT: de Kievit, Teresa
: TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
: TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
: FILE REFERENCE: 6580-089
: CURRENT APPLICATION NUMBER: US/08/846,762A
: CURRENT FILING DATE: 1997-04-30
: NUMBER OF SEQ ID NOS: 100
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 92
:
: LENGTH: 341
: TYPE: PRRT
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; ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92

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Best Local Similarity 24.0%; Fred. No. 0.62;
Matches 31; Conservative 20; Mismatches 51; Indels 27; Gaps 4

QY 47 GISPVRRTCTCTVETEDLLFVTLTLMVIELNNGGIENTLEKEVMQDYSSYFDIFLAVF 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 233 GMDITRPFPCWLLILGTFIVDATWTLVARVVGGR-----YEAARSHG--YQIASR 282
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 107 RFKTLILAAVACRLRHWWAIALTTAAVTSAPFLAKVILSKTSQGAFGVLPILISFTLMI 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 283 RFK-----RHLPVLTSAAINITWTFPIALLAGL-----NIVNPIIALIISYI 325
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 ETWFLDFKV 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 326 PLLVYIDYKL 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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: RESULT 4
: US-09-489-039A-9711
: Sequence 9711, Application US/09489039A
: Patent No. 6610836
: GENERAL INFORMATION:
: APPLICANT: Gary Breton et. al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
: TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709, 20040001
: CURRENT APPLICATION NUMBER: US/09/489,039A
: CURRENT FILING DATE: 2000-01-27
: PRIOR APPLICATION NUMBER: US 60/117,747
: PRIOR FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 14342
: SEQ ID NO 9711
: LENGTH: 350
: TYPE: PRT
: ORGANISM: Klebsiella pneumoniae
: US-09-489-039A-9711

```

```

Query Match 6.7%: Score 80.5; DB 4, Length 350;
Best Local Similarity 31.8%; Pred. No. 1.1;
Matches 21, Conservative 15, Mismatches 21, Indels 9, Gaps 3,
QY 111 LTLAAVCRLEHMAIALTTAVTSAPFLAKIYLSK-----PSQAFGVYLPILIS--IL 163
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB 83 LTLAIVSLPLPMPMMVVLGIAF--AVYIAKOLYGLGHPNPAMIGIVLILISPPVQMT 140
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 164 AMIETW 169
      :::::
DB 141 SWLPSY 146

```

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1  RESULT 5
2  US-09-171-699-4
3  ; Sequence 4, Application US/09171699
4  ; Patent No. 6448389
5  ;
6  ; GENERAL INFORMATION:
7  ;
8  ; APPLICANT: The Wistar Institute of, Anatomy & Biology
9  ;
10 ;
11 ; Gonczol, Eva
12 ; Berencsi, Klara
13 ; Karl, Csaba
14 ;
15 ; TITLE OF INVENTION: No. 6448389e1 Cytomegalovirus DNA Constructs and
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[illegible]



SEQ ID NO 14  
LENGTH: 766  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-653-14

Query Match  
Best Local Similarity 18.0%; Pred. No. 5.7; Length 766;  
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTPLDILFVTLMIIEILNVNGIENLEKEVMQDYSSYFDIFLLAVFRFKVLI-----112  
DB 13 FMSVDCVTIAIVF-----SHLDRSLIEDIRHFNIPDSVLDMAACLYRSCLLGATIG 67  
QY 113 ----LAVAVCRRL-HMMALITTAIVTSAPFLAVIISKLSQ-----GAFGY 154  
DB 68 VAKNSALGPRRLASMLVITLVCLEPGIYAMVKLL--LPSEVRPRIPDPWFALFWMTY 124  
QY 155 VLPIISFILAMIEFWLDFKVLPOEABEENRLLIVODASERALLIPGSLSDGQFY-----209  
DB 125 ISLGASFLMLWL-----LSTVRGCTQ--ALFQALTEAGFPQSGR 163  
QY 210 SPPEASGAS 218  
DB 164 PPPEQASGA 172

RESULT 12  
US-09-724-653-15  
Sequence 15, Application US/09724653  
Patent No. 6830913  
GENERAL INFORMATION:  
APPLICANT: Ling, Victor  
TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF  
FILE REFERENCE: APZ-004CP  
CURRENT APPLICATION NUMBER: US/09/724,653  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 60/167,930  
PRIOR FILING DATE: 1999-11-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 766  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-653-15

Query Match  
Best Local Similarity 18.0%; Pred. No. 5.7; Length 766;  
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTPLDILFVTLMIIEILNVNGIENLEKEVMQDYSSYFDIFLLAVFRFKVLI-----112  
DB 13 FMSVDCVTIAIVF-----SHLDRSLIEDIRHFNIPDSVLDMAACLYRSCLLGATIG 67  
QY 113 ----LAVAVCRRL-HMMALITTAIVTSAPFLAVIISKLSQ-----GAFGY 154  
DB 68 VAKNSALGPRRLASMLVITLVCLEPGIYAMVKLL--LPSEVRPRIPDPWFALFWMTY 124  
QY 155 VLPIISFILAMIEFWLDFKVLPOEABEENRLLIVODASERALLIPGSLSDGQFY-----209  
DB 125 ISLGASFLMLWL-----LSTVRGCTQ--ALFQALTEAGFPQSGR 163  
QY 210 SPPEASGAS 218  
DB 164 PPPEQASGA 172

RESULT 13  
US-09-248-796A-20444  
Sequence 20444, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 20444  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-20444

Query Match  
Best Local Similarity 22.1%; Pred. No. 1.2; Length 228;  
Matches 32; Conservative 32; Mismatches 49; Indels 32; Gaps 7;

QY 63 LRFVTL-----LMIIEILNVN--GIENLEKEVMQDYSSYF-----DIFLLAVR 106  
DB 91 LVFTALTSGAFWLSFPAINIPFGILAAQKMDTSLASLAFYLAMALISPIFMLTF 150  
QY 107 RPKVILAVAVCRRLHMMALITTAIVTSAPFLAVIISKLSQSGAGFYVPIISF-----161  
DB 151 KSTVLSGFFLC-----LTALFSLASISYFVSVALTK--MAGARVIAVVALDTFA 202  
QY 162 ILAMIEFWLDFKVL--QEAEE 183  
DB 203 LATKQNSYFTLPVILPGEAKQE 227

RESULT 14  
US-09-270-767-43373  
Sequence 43373, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 43373  
LENGTH: 251  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-43373

Query Match  
Best Local Similarity 18.8%; Pred. No. 1.3; Length 251;  
Matches 34; Conservative 46; Mismatches 63; Indels 38; Gaps 6;

QY 5 PEDMENAL--TSGQSSHASIRNHSINPQMARISYBEREKGISDVARTCLPTFD 62  
DB 51 PDSADNAVIESGIQSNLDVQGDIN--RPTDLSLAE--KKDAADRKTGTFTDAF 103  
QY 63 LRFVTLMIIEILNVNGIENLEKEVMQDYSSYFDIFLLAVFRFKVLIILAVAVCRRLH 122  
DB 104 TASIVILTELG-----DITFPIAAMARHRLIYFGALAA-----141  
QY 123 WMAIALTTAVTSAPFLAVIISKLSQSGAGFYVPIISFILAMIEFWLDFKVLPOEABE 182  
DB 142 --ALAMTILISCAFGMAANFPIKTYT-----YISTALFPIFGIKMLYDGYKMKPTDAQE 194  
QY 183 E 183  
DB 195 E 195

RESULT 15  
US-08-833-752-9  
; Sequence 9, Application US/08833752  
; Patent No. 6448375  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; APPLICANT: PARENTIER, MARC  
; APPLICANT: VASSART, GILBERT  
; APPLICANT: LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,752  
; FILING DATE: 9-APR-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6448375e  
; US-08-833-752-9

Query Match 6.5%; Score 78; DB 4; Length 355;  
Best Local Similarity 23.2%; Pred. No. 2.2;  
Matches 39; Conservative 25; Mismatches 60; Indels 44; Gaps 7;  
QY 62 DLEFVTL--WI-IELNVNGIENWLEKEWMOYDY---YSSYFDIFLAVFRKVLILAY 115  
| | | | | : | : | : | : | | | | : : |  
DB 80 DLEFIFLTPWIDYKLDQDMVFGDMCKIISGFYTGYSIFPIILITIDRIALVHAV 139  
| | | | | : | : | : | : | | | | : : |  
QY 116 AVCRLRH-----WMAIALTTAVTSAPL-----IAKVILSK 145  
| | | | | : | : | : | : | | | | : : |  
DB 140 FAIRARFVTFGVTSITIMAIATIASMPGLYFSKTYQEFTHHTCSLHFPHESLREWKLFPQ 159  
| | | | | : | : | : | : | | | | : : |  
QY 146 LPSOGAGVYLPIISFLAWIETWFLDKVLPOAEEN---RLLYV 189  
| | | | | : | : | : | : | | | | : : |  
DB 200 ALKALNLFGLVPLVLMILICYIGI---IKILLRRPNKSKSAVRLIFV 243  
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Search completed: May 17, 2005, 10:22:40  
Job time : 37 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: May 17, 2005, 10:16:30 ; Search time 63 Seconds  
(without alignments)  
1902.008 Million cell updates/sec

Title: US-10-063-518-14  
Perfect score: 1195  
Sequence: 1 MNTLPEMDNALTGSSQSHA.....EAGSEAEKQDSEKPLLEL 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Listing first 1500 summaries

Database : Uniprot 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	234	1 MENT_HUMAN	Q95772 homo sapien
2	1134.5	94.9	235	1 MENT_MOUSE	Q95413 mus musculu
3	796	66.6	227	2 Q6DI38	Q6DI38 brachydanio
4	700.5	58.6	448	2 Q6DER7	Q6DER7 xenopus tro
5	698.5	58.5	444	2 Q6PF40	Q6PF40 xenopus lae
6	684	57.2	448	2 Q6GNT3	Q6GNT3 xenopus lae
7	664	55.6	445	1 ML64_HUMAN	Q14849 homo sapien
8	656.5	54.9	446	1 ML64_MOUSE	Q61542 mus musculu
9	632	52.9	448	2 Q6PH03	Q6PH03 brachydanio
10	492	41.2	107	2 Q8BWP8	Q8BWP8 m mus muscu
11	348	29.1	568	2 Q7QIR3	Q7QIR3 anopheles g
12	343	28.7	545	2 Q8MZ44	Q8MZ44 drosophila
13	343	28.7	583	2 Q9W145	Q9W145 drosophila
14	204	17.1	447	2 Q19819	Q19819 caenorhabdi
15	104.5	8.7	294	1 ML64_SALPO	Q90289 salvelinus
16	102.5	8.6	348	2 Q97YQ0	Q97YQ0 eulicidobus
17	93.5	7.8	424	2 Q9U2W1	Q9U2W1 pyrococcus
18	93.5	7.8	564	2 Q8HQ10	Q8HQ10 thirids imag
19	91	7.6	246	2 Q8DU10	Q8DU10 streptococc
20	91	7.6	525	2 Q7VPT4	Q7VPT4 helicobacte
21	91	7.6	651	2 Q8DZK0	Q8DZK0 streptococc
22	91	7.6	651	2 Q8ESW0	Q8ESW0 streptococc
23	90.5	7.6	262	2 Q7NBJ4	Q7NBJ4 mycoplasma
24	90	7.5	1911	2 Q02038	Q02038 cyanea capi
25	89.5	7.5	233	2 Q6JCT3	Q6JCT3 aleurodicus
26	89.5	7.5	367	2 Q8HEH8	Q8HEH8 varroa dest
27	89.5	7.5	376	2 Q6JCT6	Q6JCT6 aleurodicus
28	89.5	7.5	488	2 Q840W7	Q840W7 streptococc
29	89	7.4	373	2 Q7RTB5	Q7RTB5 plasmodium
30	88.5	7.4	384	2 Q6MNV4	Q6MNV4 xana catesb
31	87	7.3	304	2 Q640B5	Q640B5 xenopus lae

32	87	7.3	610	2 Q7RRS2	Q7RRS2 plasmodium
33	87	7.3	707	2 Q6GN42	Q6GN42 xenopus lae
34	86.5	7.2	720	2 Q8PYM2	Q8PYM2 methanocarc
35	86.5	7.2	328	2 Q7NLL9	Q7NLL9 gloebacter
36	86.5	7.2	605	2 Q7Z205	Q7Z205 caenorhabdi
37	86.5	7.2	891	2 Q8UJA2	Q8UJA2 ectromelia
38	86	7.2	1050	2 Q871G6	Q871G6 neurospora
39	86	7.2	1056	2 Q7S7L6	Q7S7L6 neurospora
40	85.5	7.2	174	2 P97067	P97067 salmonella
41	85.5	7.2	336	2 Q95086	Q95086 homo sapien
42	85.5	7.2	339	2 Q95089	Q95089 homo sapien
43	85.5	7.2	336	2 Q9PME5	Q9PME5 campylobact
44	85.5	7.2	438	1 CLN3_HUMAN	CLN3266 homo sapien
45	85.5	7.2	473	1 P5S1_HUMAN	P48651 homo sapien
46	85.5	7.2	747	1 Q93GL8	Q93GL8 salmonella
47	85	7.1	348	2 Q9SFL7	Q9SFL7 arabidopsis
48	85	7.1	377	2 Q612C1	Q612C1 bacillus an
49	85	7.1	448	2 Q51531	Q51531 borrelia bu
50	85	7.1	797	2 Q82GJ8	Q82GJ8 streptomyce
51	84.5	7.1	471	1 P5S1_MOUSE	P5S1 CR10
52	84.5	7.1	473	1 P5S1_MOUSE	P5S1 CR10
53	84.5	7.1	467	2 Q6A0E5	Q6A0E5 mus musculu
54	84.5	7.1	892	2 Q9UFP90	Q9UFP90 vaccinia vi
55	84.5	7.1	1118	2 Q65U88	Q65U88 manheimela
56	84	7.0	469	2 Q9HJX8	Q9HJX8 thermoplasma
57	84	7.0	493	2 Q7TSJ7	Q7TSJ7 mus musculu
58	84	7.0	1700	2 Q75JN1	Q75JN1 dicystoscel
59	83.5	7.0	275	2 Q8XIT3	Q8XIT3 clostridium
60	83.5	7.0	303	2 Q6FNB8	Q6FNB8 candida gla
61	83.5	7.0	332	2 Q8LB40	Q8LB40 arabidopsis
62	83.5	7.0	352	2 Q97K11	Q97K11 clostridium
63	83.5	7.0	355	2 Q6K124	Q6K124 mycoplasma
64	83.5	7.0	380	2 Q97C55	Q97C55 thermoplasma
65	83.5	7.0	430	2 Q9CTA9	Q9CTA9 mus musculu
66	83.5	7.0	559	2 Q6PCX2	Q6PCX2 mus musculu
67	83.5	7.0	642	2 Q88P20	Q88P20 pseudomonas
68	83.5	7.0	834	2 Q9JHF5	Q9JHF5 mus musculu
69	83.5	7.0	834	2 Q9JL12	Q9JL12 mus musculu
70	83.5	7.0	834	2 Q91W06	Q91W06 mus musculu
71	83.5	7.0	1034	2 Q7Z2B9	Q7Z2B9 trypanosoma
72	83	6.9	238	2 Q6YR96	Q6YR96 onion yell
73	83	6.9	248	2 Q8GCS6	Q8GCS6 eubacterium
74	83	6.9	291	2 Q8ZDT0	Q8ZDT0 yersinia pe
75	83	6.9	589	2 Q7TWM1	Q7TWM1 mus musculu
76	83	6.9	580	2 Q84192	Q84192 critidia o
77	83	6.9	1056	2 Q8C2V1	Q8C2V1 mus musculu
78	83	6.9	2661	2 Q7RMS4	Q7RMS4 plasmodium
79	82.5	6.9	174	2 P97231	P97231 salmonella
80	82.5	6.9	186	2 Q7BBW2	Q7BBW2 escherichia
81	82.5	6.9	186	2 Q7BBW2	Q7BBW2 salmonella
82	82.5	6.9	239	1 Y247_MYCGE	Y24789 mycoplasma
83	82.5	6.9	341	2 Q56918	Q56918 yersinia en
84	82.5	6.9	367	2 Q8HCK3	Q8HCK3 varroa dest
85	82.5	6.9	406	2 Q87249	Q87249 laccococcus
86	82.5	6.9	419	2 Q19134	Q19134 oryctolagus
87	82.5	6.9	471	2 Q9QW77	Q9QW77 cricetus
88	82.5	6.9	510	2 Q950M6	Q950M6 rhizophydiu
89	82.5	6.9	604	2 Q8RH03	Q8RH03 fusobacteri
90	82.5	6.9	717	1 TRD1_ECOLI	TRD133 escherichia
91	82.5	6.9	717	2 Q87742	Q87742 escherichia
92	82.5	6.9	891	2 Q57223	Q57223 vaccinia vi
93	82.5	6.9	891	2 Q6J3A9	Q6J3A9 vaccinia vi
94	82.5	6.9	891	2 Q80DW2	Q80DW2 campox viru
95	82.5	6.9	892	2 Q6RZK3	Q6RZK3 rabbitpox v
96	82.5	6.9	894	2 Q8QWU0	Q8QWU0 campox viru
97	82.5	6.9	1022	2 Q88VU0	Q88VU0 lactobacilli
98	82	6.9	156	2 Q81501	Q81501 hepatitis c
99	82	6.9	161	2 Q69UD2	Q69UD2 oryza sativ
100	82	6.9	303	2 Q8RLZ3	Q8RLZ3 haemophilus
101	82	6.9	303	2 Q8RLZ3	Q8RLZ3 haemophilus
102	82	6.9	461	2 Q6AIB8	Q6AIB8 leishonia x
103	82	6.9	472	2 Q70J50	Q70J50 haemophilus
104	82	6.9	587	2 Q6C0H8	Q6C0H8 yarrowia li

105	82	6.9	589	1	RGPI_MOUSE	P46061	mus musculus	178	80	6.7	300	2	Q9CG40	Q9CG40	arabidopsis
106	82	6.9	589	2	Q91YS2	Q91YS2	mus musculus	179	80	6.7	309	1	RTM1_YEAST	P40113	saccharomyc
107	82	6.9	589	2	O8C2R3	O8C2R3	mus musculus	180	80	6.7	343	1	Q7UBB9	Q7UBB9	rhodospirill
108	82	6.9	589	2	O6NZB5	O6NZB5	mus musculus	181	80	6.7	347	2	Q9FFM1	Q9FFM1	arabidopsis
109	82	6.9	646	2	O6ZPH4	O6ZPH4	mus musculus	182	80	6.7	355	2	Q7JJA5	Q7JJA5	treponema d
110	82	6.9	647	2	O8PXU3	O8PXU3	mus musculus	183	80	6.7	359	2	Q7N4F8	Q7N4F8	phototrichu
111	82	6.9	989	2	O6CDB6	O6CDB6	Yarrowia l1	184	80	6.7	360	2	Q9H1X3	Q9H1X3	homo sapien
112	82	6.9	1031	2	O81S64	O81S64	plasmodium	185	80	6.7	388	2	O58427	O58427	pyrococcus
113	82	6.9	1466	2	P78576	P78576	emeritella	186	80	6.7	448	2	O650S8	O650S8	oryza sativ
114	81.5	6.8	190	2	O9K1A9	O9K1A9	escherichia	187	80	6.7	540	2	O6FXI7	O6FXI7	candida gla
115	81.5	6.8	297	2	O9B893	O9B893	schistosoma	188	80	6.7	650	2	O699F8	O699F8	anopheles g
116	81.5	6.8	311	2	O8CD14	O8CD14	mus musculus	189	80	6.7	661	2	Q759Y6	Q759Y6	ahlyra goss
117	81.5	6.8	349	1	RNFD_PASNU	RNFD_PASNU	pasteurella	190	80	6.7	680	2	Q7VH08	Q7VH08	helicobacte
118	81.5	6.8	352	2	O9H7E5	O9H7E5	homo sapien	191	80	6.7	700	2	Q720Z1	Q720Z1	listeria mo
119	81.5	6.8	387	2	O72CJ7	O72CJ7	desulfovibr	192	80	6.7	3010	2	Q9Q1Y9	Q9Q1Y9	hepatitis c
120	81.5	6.8	414	2	O6PAM4	O6PAM4	mus musculus	193	80	6.7	269	2	Q722B0	Q722B0	listeria mo
121	81.5	6.8	438	2	O35934	O35934	mus musculus	194	80	6.7	307	2	O89NC2	O89NC2	bradyrhizob
122	81.5	6.8	438	2	O8CSB1	O8CSB1	mus musculus	195	80	6.7	367	2	O8ESY3	O8ESY3	oceanobacti
123	81.5	6.8	447	2	Q7VRCO	Q7VRCO	candidatus	196	80	6.7	391	2	O6T196	O6T196	xiphinema a
124	81.5	6.8	465	2	O803C9	O803C9	brachydanio	197	80	6.7	438	1	CLN3_CANFA	CLN3_CANFA	causis fami
125	81.5	6.8	519	2	O9NVS8	O9NVS8	homo sapien	198	80	6.7	463	2	Q92E13	Q92E13	listeria in
126	81.5	6.8	577	2	O6P1Z6	O6P1Z6	homo sapien	199	80	6.7	488	2	O6QU70	O6QU70	aspergillus
127	81.5	6.8	577	2	O7Z748	O7Z748	homo sapien	200	80	6.7	491	1	V1B1_HCMVT	V1B1_HCMVT	human cytom
128	81.5	6.8	645	2	O67UQ9	O67UQ9	oryza sativ	201	80	6.7	546	1	FVR2_RAT	FVR2_RAT	rattus norv
129	81.5	6.8	716	2	O8DLB4	O8DLB4	synecchococ	202	80	6.7	558	2	O51954	O51954	borrelia be
130	81.5	6.8	735	2	O6B3Y6	O6B3Y6	escherichia	203	80	6.7	649	2	O6BZ08	O6BZ08	debaromyce
131	81.5	6.8	892	2	O8V2P5	O8V2P5	camelipox vi	204	80	6.7	674	2	O86P19	O86P19	drosophila
132	81.5	6.8	892	2	O75SR6	O75SR6	camelipox vi	205	80	6.7	726	2	Q9EUI3	Q9EUI3	salmonella
133	81.5	6.8	1092	2	O755K6	O755K6	ahlyra goss	206	80	6.7	784	2	Q9VYU0	Q9VYU0	drosophila
134	81.5	6.8	1480	2	Q7R386	Q7R386	giardia lam	207	80	6.7	784	2	O8KDB0	O8KDB0	chlorobact
135	81	6.8	385	2	O9ZQ69	O9ZQ69	arabidopsis	208	80	6.7	3409	2	O7S1Z7	O7S1Z7	neurospora
136	81	6.8	410	2	O6D043	O6D043	erwinia car	209	80	6.6	114	2	O6VRR6	O6VRR6	helicobacte
137	81	6.8	486	2	O63E77	O63E77	erwinia car	210	80	6.6	251	2	O6M012	O6M012	methanococ
138	81	6.8	520	1	YOU1_CABEL	YOU1_CABEL	baecillus ce	211	80	6.6	300	2	O80ZK3	O80ZK3	arvicantocis
139	81	6.8	532	1	YHB7_YEAST	YHB7_YEAST	caenorhabdi	212	80	6.6	308	2	O8RCM6	O8RCM6	fusobacteri
140	81	6.8	805	2	O8XST5	O8XST5	saccharomyc	213	80	6.6	312	2	O6KX29	O6KX29	mycoplasma
141	81	6.8	3010	2	O8QRU8	O8QRU8	hepatocitis c	214	80	6.6	323	2	O7KX19	O7KX19	drosophila
142	80.5	6.7	174	2	P97066	P97066	salmonella	215	80	6.6	349	1	RNFD_BUCAP	RNFD_BUCAP	buchnera ap
143	80.5	6.7	242	2	O8TNE9	O8TNE9	methanosaar	216	80	6.6	356	2	O7MG43	O7MG43	vibrio vuln
144	80.5	6.7	322	2	O9SNB5	O9SNB5	arabidopsis	217	80	6.6	375	2	O887L9	O887L9	pseudomonas
145	80.5	6.7	353	1	ML1A_PHOSU	PA9217	phodopsis su	218	80	6.6	484	2	O6N1E0	O6N1E0	corynebacte
146	80.5	6.7	366	2	O86KX8	O86KX8	dictyosteli	219	80	6.6	770	2	O64OD3	O64OD3	bacteroides
147	80.5	6.7	396	2	O9SU09	O9SU09	schizosacch	220	80	6.6	1531	2	O96L95	O96L95	homo sapien
148	80.5	6.7	417	1	TNAB_PROVU	P28785	proteus vul	221	80	6.6	1679	2	O86TBS	O86TBS	homo sapien
149	80.5	6.7	463	2	O8Y988	O8Y988	listeria mo	222	80	6.6	3010	2	O9J3H8	O9J3H8	hepatitis c
150	80.5	6.7	463	2	O722Q4	O722Q4	listeria mo	223	80	6.6	3010	2	O9Q1Z0	O9Q1Z0	hepatitis c
151	80.5	6.7	486	2	O9G861	O9G861	malawimonas	224	80	6.6	239	1	Y247_MYCPN	Y247_MYCPN	mycoplasma
152	80.5	6.7	536	1	MYIN_CHLTR	O63378	chlamydia c	225	80	6.6	359	2	O92DI5	O92DI5	listeria in
153	80.5	6.7	548	2	O7RC45	O7RC45	plasmodium	226	80	6.6	313	2	O9LOB3	O9LOB3	streptomyce
154	80.5	6.7	599	2	O91MB6	O91MB6	human rotav	227	80	6.6	358	1	RNFD_HAEIN	RNFD_HAEIN	haemophilus
155	80.5	6.7	644	1	YNL5_YEAST	P53925	saccharomyc	228	80	6.6	380	2	O8A6F8	O8A6F8	bacteroides
156	80.5	6.7	644	2	O6B2V3	O6B2V3	saccharomyc	229	80	6.6	382	2	O64V54	O64V54	bacteroides
157	80.5	6.7	732	2	O6S1Z5	O6S1Z5	escherichia	230	80	6.6	418	2	O65LP8	O65LP8	baecillus l1
158	80.5	6.7	738	1	TRD2_ECOLI	P22708	escherichia	231	80	6.6	451	2	O65UD5	O65UD5	manheimia
159	80.5	6.7	738	2	O7AK62	Q7AK62	plasmid r10	232	80	6.6	471	1	SH2A_CRIGR	SH2A_CRIGR	cricketulla
160	80.5	6.7	891	1	VP4A_VACCC	P20642	vaccinia vi	233	80	6.6	512	2	O8G1D7	O8G1D7	bruceila su
161	80.5	6.7	891	1	VP4A_VACCV	P16715	vaccinia vi	234	80	6.6	666	1	KUP_STRAS	KUP_STRAS	streptococc
162	80.5	6.7	891	2	O8V4W5	O8V4W5	monkeypox v	235	80	6.6	678	2	O61710	O61710	mus musculus
163	80.5	6.7	891	2	O76Z05	O76Z05	vaccinia vi	236	80	6.6	681	2	O769F3	O769F3	homo sapien
164	80.5	6.7	1687	2	Q7SC49	Q7SC49	neurospora	237	80	6.6	683	2	O769F4	O769F4	homo sapien
165	80.5	6.7	1780	2	O9ZT82	O9ZT82	arabidopsis	238	80	6.6	766	1	ABCS_HUMAN	ABCS_HUMAN	homo sapien
166	80	6.7	103	2	O9RXJ3	O9RXJ3	deinococcus	239	80	6.6	769	2	O6P2Q0	O6P2Q0	homo sapien
167	80	6.7	156	2	O81513	O81513	hepatitis c	240	80	6.6	6473	2	O8IRH9	O8IRH9	plasmodium
168	80	6.7	238	2	O9YMX2	O9YMX2	caenorhabdi	241	80	6.5	188	2	O81YM2	O81YM2	baecillus an
169	80	6.7	238	2	O95KH1	O95KH1	macaca fasc	242	80	6.5	219	2	O8W2Y0	O8W2Y0	oryza sativ
170	80	6.7	255	2	O6V7H6	O6V7H6	equine arte	243	80	6.5	226	2	O7T829	O7T829	avian infec
171	80	6.7	280	2	O635R8	O635R8	baecillus ce	244	80	6.5	240	2	O9C9P6	O9C9P6	pasteurella
172	80	6.7	280	2	O731V3	O731V3	baecillus ce	245	80	6.5	245	2	P946Z5	P946Z5	clostridium
173	80	6.7	280	2	O819H0	O819H0	baecillus ce	246	80	6.5	252	2	O6B8K2	O6B8K2	gracilaria
174	80	6.7	280	2	O81MM0	O81MM0	baecillus an	247	80	6.5	259	2	O9KD13	O9KD13	baecillus ha
175	80	6.7	280	2	O6HEFS	O6HEFS	baecillus th	248	80	6.5	331	2	O96XC4	O96XC4	sulfolobus
176	80	6.7	290	2	O99UM2	O99UM2	staphylococ	249	80	6.5	339	2	O8D4K9	O8D4K9	vibrio vuln
177	80	6.7	290	2	O7A5Y6	O7A5Y6	staphylococ	250	80	6.5	360	2	O951A3	O951A3	tetrahymena

251	78	6.5	382	2	097HC3	097hc3 clostridium	324	77	6.4	650	2	08NTK4	08nuk4 staphylococ
252	78	6.5	428	2	08TN61	08tn61 methanosc	325	77	6.4	650	2	099Q27	099q27 staphylococ
253	78	6.5	428	2	08DSY9	08dsy9 vibrio vuln	326	77	6.4	650	2	07A374	07a374 staphylococ
254	78	6.5	431	2	09JRS0	09jrs0 actinobacil	327	77	6.4	650	2	06G633	06g633 staphylococ
255	78	6.5	442	2	07MD08	07md08 vibrio vuln	328	77	6.4	650	2	06G633	06g633 staphylococ
256	78	6.5	471	1	Y872 HAEIN	Y8721 haemophilus	329	77	6.4	722	2	0632R1	0632r1 bacillus ce
257	78	6.5	486	2	06HMA8	06hma8 bacillus th	330	77	6.4	788	2	08L838	08l838 arabadopsi
258	78	6.5	545	2	06FSM9	06fsm9 candida gla	331	77	6.4	789	1	FTSK STAAW	08nw8 staphylococ
259	78	6.5	641	2	09LIC2	09lic2 arabadopsi	332	77	6.4	789	2	06G9T7	06g9t7 staphylococ
260	78	6.5	650	2	07QG08	07qg08 anophelis g	333	77	6.4	836	2	07Z1F2	07z1f2 plasmodium
261	78	6.5	688	2	09BM77	09bm77 rhizobium 1	334	77	6.4	877	2	0750H8	0750h8 ashbya gos
262	78	6.5	1297	2	09Y817	09y817 schizosacch	335	77	6.4	991	2	081330	081330 arabadopsi
263	78	6.5	2136	1	YCF2 MARPO	YCF21 marchantia	336	77	6.4	1024	2	08IKZ6	08ikz6 plasmodium
264	78	6.5	7180	1	R1AB_CVMJH	R19751 m replicase	337	77	6.4	1024	2	07Z1P1	07z1p1 plasmodium
265	77.5	6.5	176	2	0976T7	0976t7 sulfolobus	338	77	6.4	1025	2	025593	025593 plasmodium
266	77.5	6.5	190	2	09K1A8	09k1a8 escherichia	339	77	6.4	1117	2	09M133	09m133 arabadopsi
267	77.5	6.5	263	2	073DX2	073dx2 bacillus ce	340	77	6.4	1477	2	06FTR9	06ftr9 candida gla
268	77.5	6.5	263	2	081I83	081i83 bacillus ce	341	77	6.4	1500	2	09ZU84	09zu84 arabadopsi
269	77.5	6.5	269	2	08Y8T5	08y8t5 listeria mo	342	77	6.4	3010	2	068788	068788 hepatitis c
270	77.5	6.5	270	2	08H1Y1	08h1y1 perognathus	343	77	6.4	3010	2	081757	081757 hepatitis c
271	77.5	6.5	270	2	08H1Y2	08h1y2 perognathus	344	77	6.4	3010	2	09J3G4	09j3g4 hepatitis c
272	77.5	6.5	270	2	08H1Y3	08h1y3 perognathus	345	77	6.4	3013	2	06J6P5	06j6p5 hepatitis c
273	77.5	6.5	270	2	08H1Y4	08h1y4 perognathus	346	77	6.4	4416	2	09J3F8	09j3f8 murine hepa
274	77.5	6.5	294	2	08E130	08e130 oceanobacil	347	77	6.4	4416	2	09J3F8	09j3f8 murine hepa
275	77.5	6.5	299	2	066FT9	066ft9 yersinia ps	348	77	6.4	7124	1	R1AB_CVM2	09pya3 m replicase
276	77.5	6.5	329	2	08ZAL1	08zal1 yersinia pe	349	77	6.4	278	2	08XBFO	08xbfo escherichia
277	77.5	6.5	310	2	08D1I6	08d1i6 yersinia pe	350	76.5	6.4	281	2	08SKS9	08sk9 ancylostoma
278	77.5	6.5	327	2	09PQJ1	09pqj1 ureaplasma	351	76.5	6.4	282	2	09ZNV5	09znv5 rhizobium m
279	77.5	6.5	328	2	09K6B6	09k6b6 bacillus ha	352	76.5	6.4	342	2	07Z290	07z290 caenorhabd
280	77.5	6.5	338	2	042882	042882 schizosacch	353	76.5	6.4	352	1	RNPD_SALT1	08z6g8 salmonella
281	77.5	6.5	365	2	08R770	08r770 thermoaer	354	76.5	6.4	352	1	RNPD_SALT1	08z6g8 salmonella
282	77.5	6.5	379	2	048008	048008 perognathus	355	76.5	6.4	379	1	CYB_DIPOR	08gaw3 dipodomys o
283	77.5	6.5	392	2	08G7P7	08g7p7 bifidobacte	356	76.5	6.4	379	2	09GBY7	09gby7 ochocrona pa
284	77.5	6.5	411	2	09P6N5	09p6n5 schizosacch	357	76.5	6.4	380	2	08HN17	08hn17 psomyia nat
285	77.5	6.5	422	2	09HKX6	09hxx6 thermoplas	358	76.5	6.4	395	2	08KHK2	08khk2 pseudomonas
286	77.5	6.5	440	2	09ZYX3	09zyx3 pedinomonas	359	76.5	6.4	415	2	07UB13	07ub13 shigella fl
287	77.5	6.5	458	2	06ZXT1	06zxt1 bacillus li	360	76.5	6.4	415	2	083PL5	083pl5 shigella fl
288	77.5	6.5	481	2	09G8V8	09g8v8 rhodomomas	361	76.5	6.4	438	1	CLN3 MOUSE	06l124 mus musculu
289	77.5	6.5	491	2	028284	028284 archaeoglob	362	76.5	6.4	439	2	064SNO	064sno bacteroides
290	77.5	6.5	491	2	06SX10	06sx10 human cytom	363	76.5	6.4	451	2	06EOT8	06eot8 borrelia ga
291	77.5	6.5	512	2	08YGI2	08ygi2 bruceila me	364	76.5	6.4	453	2	06ZG24	06zgv4 oryza sativ
292	77.5	6.5	556	2	089180	089180 variola vir	365	76.5	6.4	462	2	082V00	082v00 nltrosomona
293	77.5	6.5	556	2	089232	089232 variola vir	366	76.5	6.4	468	1	YDEM_CABEL	019084 caenorhabd
294	77.5	6.5	567	2	07RNKO	07rnko plasmodium	367	76.5	6.4	480	2	06SX39	06sx39 human cytom
295	77.5	6.5	620	2	08EKAL	08ekal strewnella	368	76.5	6.4	491	2	06SWP6	06swp6 human cytom
296	77.5	6.5	734	1	NU5C_ORYSA	P12129 oryza sativ	369	76.5	6.4	500	2	06ZTH3	06zth3 sulfolobus
297	77.5	6.5	892	2	VP4A_VARY	P33817 variola vir	370	76.5	6.4	526	1	FVR2_HUMAN	09upr3 homo sapien
298	77.5	6.5	892	2	09QNT0	09qnt0 variola min	371	76.5	6.4	538	2	07VP70	07vp70 haemophilus
299	77.5	6.5	979	2	07MLV5	07mlv5 vibrio vuln	372	76.5	6.4	538	2	09PIV5	09piv5 campylobact
300	77.5	6.5	1476	2	08ST66	08st66 dictyostei	373	76.5	6.4	555	2	08NBG4	08nbg4 homo sapien
301	77.5	6.5	1784	2	025377	025377 loligo opal	374	76.5	6.4	570	2	07Z6J6	07z6j6 homo sapien
302	77.5	6.5	2141	2	0869H2	0869h2 lymanea sta	375	76.5	6.4	589	2	09ZLNL1	09zlnl1 helicobacte
303	77	6.4	170	2	072UC4	072uc4 leptospira	376	76.5	6.4	614	2	08FWB2	08fwb2 bruceila su
304	77	6.4	170	2	08FO04	08fo04 leptospira	377	76.5	6.4	649	2	06KZL4	06kzl4 dicryphi
305	77	6.4	255	2	098VNS	098vns equine arte	378	76.5	6.4	687	2	074520	074520 schizosacch
306	77	6.4	286	2	06I082	06i082 bacillus an	379	76.5	6.4	743	2	08XN80	08xn80 clostridium
307	77	6.4	286	2	073A28	073a28 bacillus ce	380	76.5	6.4	839	2	0918C9	0918c9 gallus gall
308	77	6.4	353	1	09XTH3	09xth3 caenorhabd	381	76.5	6.4	909	2	08T9W6	08t9w6 dictyostei
309	77	6.4	353	1	ML1A_MOUSE	06l184 mus musculu	382	76.5	6.4	1485	2	08EU2A	08eu2a mycoplaema
310	77	6.4	379	2	08WKE6	08wke6 thomomys ta	383	76.5	6.4	1641	2	06BS27	06bs27 debaryomyce
311	77	6.4	383	2	08TZC2	08tzc2 methanopyru	384	76.5	6.4	156	2	081504	081504 hepatitis c
312	77	6.4	386	2	07MX00	07mx00 porphyromon	385	76.5	6.4	201	2	06MT09	06mt09 mycoplaema
313	77	6.4	419	2	P94949	P94949 methanopyru	386	76.5	6.4	210	2	08PX10	08px10 methanosc
314	77	6.4	423	2	071X58	071x58 listeria mo	387	76.5	6.4	255	2	06V715	06v715 equine arte
315	77	6.4	430	2	08ULZ6	08ulz6 treponema d	388	76.5	6.4	272	2	08R7J2	08r7j2 thermoaer
316	77	6.4	435	2	073RD9	073rd9 treponema d	389	76.5	6.4	292	2	08ELU4	08elu4 oceanobacil
317	77	6.4	444	2	08NYSX	08nysx staphylococ	390	76.5	6.4	325	2	09Z2H9	09z2h9 mesocricetu
318	77	6.4	444	2	06CD70	06cd70 staphylococ	391	76.5	6.4	342	1	NU2M_LOCM1	036426 locusta mig
319	77	6.4	490	2	014670	014670 homo sapien	392	76.5	6.4	402	2	0219J3	0219j3 caenorhabd
320	77	6.4	491	2	09T251	09t251 phytophthor	393	76.5	6.4	425	2	09URS2	09ur52 actinobacil
321	77	6.4	519	2	09ASQ7	09asq7 arabadopsi	394	76.5	6.4	438	2	08BHG7	08bhg7 pseudomonas
322	77	6.4	559	2	09AAX4	09aax4 culbacter	395	76.5	6.4	461	2	085002	085002 streptococ
323	77	6.4	590	1	NU5M_TRYBB	P04540 trypanosoma	396	76.5	6.4	474	2	07ZSX4	07zsx4 leptospira

397	76	6.4	474	2	O8F2K0	O8f2k0 leptospi	470	75	6.3	132	2	Q6N505	O6n505 rhodopseudo
398	76	6.4	519	2	O852P3	O852p3 perilla fru	471	75	6.3	156	2	O81498	O81498 hepatitis c
399	76	6.4	567	2	O6NXT6	O6nxt6 homo sapien	472	75	6.3	156	2	O81507	O81507 hepatitis c
400	76	6.4	616	2	O7OWH6	O7owh6 giardia lam	473	75	6.3	156	2	O81531	O81531 hepatitis c
401	76	6.4	669	2	O9LZ27	O9lzz2 arabidopsis	474	75	6.3	215	2	O34238	O34238 capricornis
402	76	6.4	699	2	O6IVM6	O6ivm6 uncultured	475	75	6.3	218	2	O6SKR1	O6skr1 arthrobacte
403	76	6.4	851	2	O6CK04	O6ck04 kluyveromyc	476	75	6.3	225	2	O6VMD0	O6vmd0 avian infec
404	76	6.4	931	2	O7NENO	O7nbno mycoplasma	477	75	6.3	227	2	O9GAT3	O9gat3 ochotona hy
405	76	6.4	1252	1	O7PVU9	O7pvu9 anopheles g	478	75	6.3	249	1	YD68 METJA	O58763 methanococ
406	76	6.4	1301	1	DHX9 CAEBL	O22307 caenorhabdi	479	75	6.3	256	2	O631U3	O631u3 bacillus ce
407	76	6.4	1450	1	CCTR_RABIT	O00554 oryctolagus	480	75	6.3	274	2	O9KND0	O9knd0 vibrio chol
408	76	6.4	1481	2	O9TX9	O9tx9 oryctolagus	481	75	6.3	277	2	O6MNA3	O6mna3 bdellovibri
409	76	6.4	1551	2	O96WNA	O96wna venturia in	482	75	6.3	294	2	O8RET4	O8ret4 fusobacteri
410	76	6.4	1783	2	O18698	O18698 caenorhabdi	483	75	6.3	302	2	O6CWK2	O6cwk2 kluyveromyc
411	76	6.4	1877	2	O8MOA1	O8mga1 caenorhabdi	484	75	6.3	330	2	O58239	O58239 pyrococcus
412	76	6.4	2009	2	O7RRB2	O7rrb2 plasmodium	485	75	6.3	371	2	O8BW45	O8bw45 mus musculu
413	76	6.4	3010	2	P90191	P90191 hepatitis c	486	75	6.3	373	1	PE23 PTG	P50131 sus scrofa
414	76	6.4	3010	2	P90193	P90193 hepatitis c	487	75	6.3	380	1	CYB_RANRU	O9f6f3 rana rugosa
415	76	6.4	3010	2	P90194	P90194 hepatitis c	488	75	6.3	380	2	O6G6U2	O6g9j2 nandus nebu
416	75.5	6.3	156	1	ML1A RAT	P49218 rattus norv	489	75	6.3	387	2	O46657	O46657 sus scrofa
417	75.5	6.3	162	2	O6PFG7	O6ppg7 rattus norv	490	75	6.3	407	2	O7NRF5	O7nrf5 chromobacte
418	75.5	6.3	220	2	O633A3	O633a3 bacillus ce	491	75	6.3	418	2	O6ORF8	O6ofr8 legionella
419	75.5	6.3	228	2	O9VUN8	O9vun8 drosophila	492	75	6.3	418	2	O6A8T1	O6atr1 propionibac
420	75.5	6.3	231	2	O6MD11	O6md11 paracitlamyd	493	75	6.3	460	2	O62CF6	O62cf6 burkholderi
421	75.5	6.3	244	2	O6B927	O6b927 gracillaria	494	75	6.3	460	2	O63QA3	O63q43 burkholderi
422	75.5	6.3	247	2	O7TP13	O7tp13 rattus norv	495	75	6.3	473	1	GAR1 HUMAN	P24046 homo sapien
423	75.5	6.3	248	2	O63EZ9	O63ez9 bacillus ce	496	75	6.3	488	2	O7RMW8	O7rmw8 neurospora
424	75.5	6.3	248	2	O6HMF5	O6hmf5 bacillus th	497	75	6.3	496	2	O75U67	O75u67 fuigu rubrip
425	75.5	6.3	263	2	O63GB2	O63gb2 bacillus ce	498	75	6.3	498	2	O9SN21	O9sn21 arabidopsis
426	75.5	6.3	263	2	O97PD2	O97pd2 streptococc	499	75	6.3	526	2	O7NS50	O7nse2 bacillus su
427	75.5	6.3	263	2	O81YU8	O81yu8 bacillus an	500	75	6.3	543	2	O7NS50	O7ns50 chromobacte
428	75.5	6.3	263	2	O8CYF4	O8cyf4 streptococc	501	75	6.3	649	2	O34952	O34952 bacillus su
429	75.5	6.3	263	2	O6HNS6	O6hns6 bacillus th	502	75	6.3	753	2	O7VED4	O7ved4 prochloroto
430	75.5	6.3	269	2	O6PFG6	O6ppg6 xenopus lae	503	75	6.3	777	2	O98G59	O98g59 guillardia
431	75.5	6.3	278	2	O86SK7	O86sk7 macropus eu	504	75	6.3	885	2	O8PUI6	O8pui6 paramecium
432	75.5	6.3	303	2	O8KZ08	O8kz08 streptomyce	505	75	6.3	937	2	O82ZU7	O82zr7 methanobarc
433	75.5	6.3	310	2	O87OH5	O87oh5 saccharomyc	506	75	6.3	1008	2	O89152	O89152 hepatitis c
434	75.5	6.3	326	2	O9ESJ3	O9esj3 rattus norv	507	75	6.3	1008	2	O89153	O89153 hepatitis c
435	75.5	6.3	339	2	O9SKB3	O9skb3 vibrio chol	508	75	6.3	1008	2	O89156	O89156 hepatitis c
436	75.5	6.3	342	2	O9QEV3	O9qev3 human herpe	509	75	6.3	1131	2	O8NAT5	O8nat5 homo sapien
437	75.5	6.3	352	1	RNFD_ECOLI	P58125 escherichia	510	75	6.3	1145	2	O8GUB7	O8gub7 cymodocea n
438	75.5	6.3	352	1	RNFD_ECOLI	P76182 escherichia	511	75	6.3	1154	2	O6PRT6	O6prt6 candida gla
439	75.5	6.3	352	1	O8F9H4	O8f9h4 escherichia	512	75	6.3	1336	2	O6F1U1	O6f1u1 mesoplasma
440	75.5	6.3	352	2	O83KY5	O83ky5 shigella fl	513	75	6.3	1336	2	O6F1U1	O6f1u1 mesoplasma
441	75.5	6.3	379	1	CYB_ZAPTR	O9xmti zapla japoni	514	75	6.3	1704	2	O95206	O95206 trypanosoma
442	75.5	6.3	389	2	O8AVS5	O8aves byla japoni	515	75	6.3	2248	1	CYAL DROME	P32871 drosophila
443	75.5	6.3	397	2	O9N4R5	O9n4r5 caenorhabdi	516	75	6.3	2248	2	O9VY17	O9vy17 drosophila
444	75.5	6.3	397	2	O6RXC2	O6rcx2 human cytom	517	75	6.3	3010	2	O68833	O68833 hepatitis c
445	75.5	6.3	410	2	O7ONM4	O7onw4 strongyloid	518	75	6.3	3010	2	O9J3G5	O9j3g5 hepatitis c
446	75.5	6.3	415	1	TNAB_ECO57	O8xb33 escherichia	519	75	6.3	3010	2	O9Q1Y7	O9q1y7 hepatitis c
447	75.5	6.3	415	1	TNAB_ECOLI	P31173 escherichia	520	75	6.3	3010	2	O9Q1Y8	O9q1y8 hepatitis c
448	75.5	6.3	415	2	O8FBV1	O8fbv1 escherichia	521	74.5	6.2	174	2	P97068	P97068 salmonella
449	75.5	6.3	433	2	O6PFC9	O6pfc9 caenorhabdi	522	74.5	6.2	179	2	O8BPH9	O8bph9 oceanobacil
450	75.5	6.3	446	2	O7S8U0	O7s8u0 neurospora	523	74.5	6.2	180	2	P71253	P71253 escherichia
451	75.5	6.3	471	1	SH2A_MOUSE	P35363 mus musculu	524	74.5	6.2	227	2	O9GAT4	O9gat4 ochotona cu
452	75.5	6.3	481	2	O8COK0	O8cok0 mus musculu	525	74.5	6.2	227	2	O9GAT5	O9gat5 ochotona th
453	75.5	6.3	482	2	O9PJ00	O9pj0 echizosacch	526	74.5	6.2	227	2	O9GAT6	O9gat6 ochotona pr
454	75.5	6.3	491	2	O6SWJ1	O6swj1 human cytom	527	74.5	6.2	258	2	O8BWC7	O8bwc7 lactobacilli
455	75.5	6.3	491	2	O6SWS4	O6sws4 human cytom	528	74.5	6.2	276	2	O8R9O5	O8r9o5 rhizobium m
456	75.5	6.3	491	2	O6SWT2	O6swt2 human cytom	529	74.5	6.2	280	2	O6WTF6	O6wtf6 synecchococ
457	75.5	6.3	491	2	O6SWT1	O6swt1 human cytom	530	74.5	6.2	290	2	O6SEU1	O6seu1 uncultured
458	75.5	6.3	498	2	O47543	O47543 chlamydomon	531	74.5	6.2	298	2	O6BWD3	O6bw3 debaryomyce
459	75.5	6.3	501	2	O6CHZ5	O6chz5 yarrowia li	532	74.5	6.2	313	2	O8RTK6	O8rtk6 thermoaer
460	75.5	6.3	551	1	PVR2_MOUSE	O91x85 mus musculu	533	74.5	6.2	335	2	O9KXST	O9kxst thermocoga
461	75.5	6.3	593	2	O2S3Z2	O2s3z2 helicobacte	534	74.5	6.2	355	1	C3X1 HUMAN	P49238 homo sapien
462	75.5	6.3	708	2	O22806	O22806 caenorhabdi	535	74.5	6.2	364	2	O81DY2	O81dy2 plasmodium
463	75.5	6.3	746	2	O8PGW4	O8pgw4 xanthomonas	536	74.5	6.2	377	2	O766W3	O766w3 varzula hil
464	75.5	6.3	773	2	O96325	O96325 arabidopsis	537	74.5	6.2	378	2	O6DUV8	O6duv8 brasica na
465	75.5	6.3	775	1	CLCA_ARATH	P92941 arabidopsis	538	74.5	6.2	379	1	CYB_OCHPR	O9bd24 ochotona pr
466	75.5	6.3	1008	2	O89154	O89154 hepatitis c	539	74.5	6.2	379	2	O8MB05	O8mb05 aplodontia
467	75.5	6.3	1142	2	O9UT41	O9ut41 schizosacch	540	74.5	6.2	392	2	O9B9E3	O9b9e3 chaetodipus
468	75.5	6.3	1583	2	O7P9E4	O7p9e4 rickettsia	541	74.5	6.2	392	2	O9LCN4	O9lcn4 micromonosp
469	75.5	6.3	3010	2	O9J3G7	O9j3g7 hepatitis c	542	74.5	6.2	442	2	O94A13	O94a13 arabidopsis

543	74.5	6.2	458	2	065MD8	065m8 bacillus li	616	74	6.2	650	2	0956S6	09566 lactococcus
544	74.5	6.2	471	1	5H2A_RAT	p14842 rattus norv	617	74	6.2	742	2	06FNV6	06fnv6 candida gla
545	74.5	6.2	473	1	09K5T9	09k5t9 bacillus ha	618	74	6.2	841	2	06ANP1	06anp1 carsonella
546	74.5	6.2	488	2	06Q0V1	06q0v1 aspergillus	619	74	6.2	846	2	093U47	093u47 carsonella
547	74.5	6.2	500	2	024348	024348 sorghum b1c	620	74	6.2	892	2	08TGB2	08tgb2 candida alb
548	74.5	6.2	540	2	066CQ5	066cq5 arabidopsis	621	74	6.2	1133	2	095S89	095s89 arabidopsis
549	74.5	6.2	562	2	026QCS	026qcs homo sapien	622	74	6.2	1123	2	09SPU7	09spu7 arabidopsis
550	74.5	6.2	574	2	022454	022454 triticum ae	623	74	6.2	3010	2	0913V3	0913v3 hepatitis c
551	74.5	6.2	597	2	03VDA0	03vda0 dtrosophila	624	74	6.2	3010	2	09DRE8	09dre8 hepatitis c
552	74.5	6.2	618	1	YKRA_YEAST	p36029 saccharomyc	625	74	6.2	3010	2	09UJH6	09ujh6 hepatitis c
553	74.5	6.2	848	1	08VVK9	08vvk9 corynebacte	626	74	6.2	3010	2	09Q1Y1	09q1y1 hepatitis c
554	74.5	6.2	990	1	FTSK_VIBU	06d8m2 vibrio vuln	627	74	6.2	3010	2	09SKA6	09ska6 hepatitis c
555	74.5	6.2	1033	2	07Z2C0	07z2c1 typanosoma	628	74	6.2	120	2	09SKA6	09ska6 arabidopsis
556	74.5	6.2	1034	2	07Z2C0	07z2c2 typanosoma	629	73.5	6.2	153	2	092XD3	092xd3 pyrobaculum
557	74.5	6.2	1183	2	094447	094447 galliphora	630	73.5	6.2	180	2	08ZXS3	08zxs3 pyrobaculum
558	74.5	6.2	1520	2	08T687	08t687 dictyostell	631	73.5	6.2	180	2	P712S1	P712s1 escherichia
559	74.5	6.2	1559	2	07S0S1	07s0s1 neurospora	632	73.5	6.2	180	2	P712S7	P712s7 escherichia
560	74.5	6.2	1808	2	091Y86	091y86 arabidopsis	633	73.5	6.2	180	2	P75018	P75018 escherichia
561	74.5	6.2	1837	2	08IKP1	08ikp1 plasmodium	634	73.5	6.2	199	2	08DVR3	08dvr3 streptococc
562	74.5	6.2	3010	2	091AU0	091au0 hepatitis c	635	73.5	6.2	216	1	YK36_AQUAE	067827 aquilex aeo
563	74	6.2	124	2	08KC46	08kc46 chlorobium	636	73.5	6.2	226	2	09J0X1	09j0x1 avian infec
564	74	6.2	156	2	081528	081528 hepatitis c	637	73.5	6.2	270	2	08HBP0	08hbp0 perognathus
565	74	6.2	167	2	08W272	08w272 homo sapien	638	73.5	6.2	270	2	08HIY6	08hiy6 perognathus
566	74	6.2	225	2	091SA2	091sa2 avian infec	639	73.5	6.2	274	2	095L51	095l51 capra hircu
567	74	6.2	230	2	088Y70	088y70 lactobacill	640	73.5	6.2	298	2	06Z2T3	06z2t3 cryza sativ
568	74	6.2	231	1	028852	027961 archaeoglob	641	73.5	6.2	318	2	055895	055895 synechocyst
569	74	6.2	231	2	028852	028852 archaeoglob	642	73.5	6.2	318	1	YYAD_BACSU	P77520 bacillus ae
570	74	6.2	238	2	06HER1	06het1 bacillus th	643	73.5	6.2	360	2	08U0M8	08u0m8 bractydantio
571	74	6.2	255	2	06C483	06c483 equine arte	644	73.5	6.2	367	2	064BD6	064bd6 uncultured
572	74	6.2	278	2	06CUI8	06cul8 kuiveteromyc	645	73.5	6.2	379	1	CYB_THOTA	035457 phoca green
573	74	6.2	286	1	P0TB_MYCPN	P75058 mycoplasma	646	73.5	6.2	379	1	09G3M8	09g3m8 thomomys ca
574	74	6.2	291	2	0669C8	0669c8 yerania ps	647	73.5	6.2	379	2	CYB_STRPU	P15547 strongyloce
575	74	6.2	294	2	09SM72	09sm72 oryza sativ	648	73.5	6.2	380	1	CYB_STRPU	P15547 strongyloce
576	74	6.2	295	1	CYOE_PSEPU	09sm75 pseudomonas	649	73.5	6.2	384	1	OPGC_SALTY	OPGC salty
577	74	6.2	295	2	06S4M3	06s4m3 pseudomonas	650	73.5	6.2	384	1	OPGC_SALTY	OPGC salty
578	74	6.2	300	1	NUZM_ASCSU	P48777 ascaris suu	651	73.5	6.2	385	2	P94442	P94442 sphingomona
579	74	6.2	312	1	PYRB_AERPE	09ch74 ascaris suu	652	73.5	6.2	387	2	09KMU2	09kmu2 porphyromon
580	74	6.2	312	2	09CH74	09ch74 lactococcus	653	73.5	6.2	387	2	07MVX5	07mvx5 macaca mula
581	74	6.2	315	2	0710S2	0710s2 epalax leuc	654	73.5	6.2	389	1	OXKR_MACMU	OXKR macmu
582	74	6.2	315	2	08M6V0	08m6v0 ligilopne j	655	73.5	6.2	391	1	OXKR_BOVIN	OXKR bovin
583	74	6.2	324	2	08DVZ6	08dvz6 streptococc	656	73.5	6.2	397	2	0822F7	0822f7 enterococcu
584	74	6.2	349	1	110S_MOUSE	061190 mus musculu	657	73.5	6.2	409	2	07V140	07v140 prochloroco
585	74	6.2	350	1	MLIA_HUMAN	P48039 homo sapien	658	73.5	6.2	413	2	09Z8T3	09z8t3 listeria in
586	74	6.2	351	2	09VM77	09vm77 mus musculu	659	73.5	6.2	421	2	08PK37	08pk37 xenomomus
587	74	6.2	354	2	06SUT4	06sut4 manihelmita	660	73.5	6.2	425	2	06DEK1	06dek1 ertwinia car
588	74	6.2	361	2	064AL9	06e4l9 uncultured	661	73.5	6.2	442	2	08GZJ4	08gzj4 arabidopsis
589	74	6.2	379	1	CYB_THOMO	08wek2 thomomys mo	662	73.5	6.2	442	2	09XIQ7	09xiq7 arabidopsis
590	74	6.2	379	2	047580	047980 thomomys bo	663	73.5	6.2	491	1	VIE1_HCMVA	P13202 human cytom
591	74	6.2	379	2	048002	048002 thomomys mo	664	73.5	6.2	491	2	06SWZ8	06swz8 human cytom
592	74	6.2	379	2	048003	048003 thomomys mo	665	73.5	6.2	491	2	07M6S4	07m6s4 human cytom
593	74	6.2	379	2	08WEK5	08wek5 thomomys ca	666	73.5	6.2	518	2	07RT44	07rt44 plasmodium
594	74	6.2	380	2	08HHU7	08hhj7 thomomys bo	667	73.5	6.2	523	2	064WT6	064wt6 bacteroides
595	74	6.2	380	2	074KX0	074kx0 lactobacill	668	73.5	6.2	557	2	08VZ62	08vz62 arabidopsis
596	74	6.2	381	1	CYB_PSENI	035553 pseudantech	669	73.5	6.2	574	2	093390	093390 candida alb
597	74	6.2	396	2	08NKC4	08nkc4 strephyllococ	670	73.5	6.2	607	2	06DRF5	06drf5 xenopus lae
598	74	6.2	396	2	093V76	093v76 strephyllococ	671	73.5	6.2	634	1	KUP_XYLPA	09pcp78 xyella fas
599	74	6.2	396	2	07ADJ3	07ad63 strephyllococ	672	73.5	6.2	637	1	MUTL_BACHD	09kaci bacillus ha
600	74	6.2	396	2	06GARI	06gari strephyllococ	673	73.5	6.2	640	1	APRN_ENTHI	P20301 entamoeba h
601	74	6.2	396	2	06G168	06g168 strephyllococ	674	73.5	6.2	653	2	08TTH1	08tth1 methanosarc
602	74	6.2	418	2	06QF89	06qf89 legionella	675	73.5	6.2	684	2	068468	068468 corynebacte
603	74	6.2	418	2	06QFCS	06qfcs legionella	676	73.5	6.2	731	2	016531	016531 caenorhabdi
604	74	6.2	418	2	06QFC7	06qfc7 legionella	677	73.5	6.2	846	2	093U53	093u53 carsonella
605	74	6.2	442	2	09CE66	09ceg6 lactococcus	678	73.5	6.2	1049	2	06FMY2	06fmy2 candida gla
606	74	6.2	457	2	08RBZ7	08rbz7 thermoanaer	679	73.5	6.2	1095	2	09C7H5	09c7h5 arabidopsis
607	74	6.2	475	2	09S2G7	09s2g7 streptococci	680	73.5	6.2	1174	2	07M006	07m006 murine hepa
608	74	6.2	485	2	09XVK0	09xvk0 caenorhabdi	681	73.5	6.2	1277	2	076G00	07yus9 drosophila
609	74	6.2	487	2	023384	023384 arabidopsis	682	73.5	6.2	1287	2	07YUS9	07yus9 drosophila
610	74	6.2	493	2	09EVJ7	09evj7 flavobacter	683	73.5	6.2	1287	2	09U5W1	09u5w1 drosophila
611	74	6.2	503	2	06M052	06m052 methanococc	684	73.5	6.2	1287	2	09V124	09v124 drosophila
612	74	6.2	528	2	06CKR2	06ckr2 kuiveteromyc	685	73.5	6.2	1292	2	09A1H0	09a1h0 carsonella
613	74	6.2	528	2	06CKR2	06ckr2 kuiveteromyc	686	73.5	6.2	1476	2	0965D3	0965d3 dictyostell
614	74	6.2	540	2	06LFP3	06lfp3 plasmodium	687	73.5	6.2	1545	2	08GUB5	08gub5 oryza sativ
615	74	6.2	581	2	06FIT6	06fit6 candida gla	688	73.5	6.2	2666	2	06FW99	06fw99 candida gla

589	73.5	6.2	3010	2	Q9DTE6	Q9dte6 hepatitis c	762	73	6.1	668	2	Q9ALX8	Q9alx8 burkholderi
590	73.5	6.2	3381	2	Q8IDK4	Q8idk4 plasmodium	763	73	6.1	668	2	Q63JL61	Q63jl61 burkholderi
591	73.5	6.2	4470	2	Q66WN5	Q66wn5 murine hepa	764	73	6.1	676	2	Q9VFP31	Q9vfp31 drosophila
592	73.5	6.2	7176	1	RIAB_CWMA5	RI6342 m replicase	765	73	6.1	788	1	FTSK_STAM	PE4164 staphylococ
593	73.5	6.2	7178	2	Q66WN6	Q66wn6 murine hepa	766	73	6.1	788	1	FTSK_STAM	PE4165 staphylococ
594	73	6.1	114	2	Q75XAV	Q75xav helicobacte	767	73	6.1	789	2	Q6GHF9	Q6ghf9 staphylococ
595	73	6.1	114	2	Q92LU2	Q92lu2 helicobacte	768	73	6.1	832	2	Q7UQP9	Q7uqp9 rhodospirill
596	73	6.1	138	2	Q97777	Q97777 elephas max	769	73	6.1	844	2	Q6KYT8	Q6kyt8 picophilus
597	73	6.1	140	2	Q64145	Q64145 rattus sp.	770	73	6.1	861	2	Q9AVX8	Q9avx8 guillardia
598	73	6.1	145	2	Q9UXB0	Q9uxb0 bulfolobus	771	73	6.1	966	1	PKD2_MOUSE	Q35245 mus musculu
599	73	6.1	155	2	Q7VJPI	Q7vjpi helicobacte	772	73	6.1	966	2	Q7TSI7	Q7tsi7 mus musculu
700	73	6.1	156	2	Q81510	Q81510 hepatitis c	773	73	6.1	966	2	Q8BPR6	Q8bpr6 mus musculu
701	73	6.1	156	2	Q81522	Q81522 hepatitis c	774	73	6.1	971	2	Q60337	Q60337 homo sapien
702	73	6.1	156	2	Q81537	Q81537 hepatitis c	775	73	6.1	1035	2	Q967W1	Q967w1 schistosoma
703	73	6.1	163	2	Q80RY8	Q80ry8 avian infec	776	73	6.1	1075	2	Q9LPE2	Q9lpe2 arabidopsis
704	73	6.1	220	2	Q72240	Q72240 bacillus ce	777	73	6.1	1111	2	Q86FP2	Q86fp2 caenorhabdi
705	73	6.1	223	1	VMEI_IBVG	Q910e2 bacillus ce	778	73	6.1	1137	2	Q9N323	Q9n323 caenorhabdi
706	73	6.1	223	1	Q91S7	Q91s7 avian infec	779	73	6.1	1931	2	Q8RJT3	Q8rjt3 stigmatella
707	73	6.1	226	2	Q7TPP6	Q91897 avian infec	780	73	6.1	2010	2	Q7PEZ7	Q7pezt7 anophelis g
708	73	6.1	238	1	PYRF_BACCR	Q719p6 avian infec	781	73	6.1	3010	2	Q88803	Q88803 hepatitis c
709	73	6.1	238	1	Q63E63	Q63e63 bacillus ce	782	73	6.1	3010	2	Q9J3G1	Q9j3g1 hepatitis c
710	73	6.1	238	2	Q73216	Q73216 bacillus ce	783	73	6.1	3010	2	Q9J3I0	Q9j3i0 hepatitis c
711	73	6.1	249	2	Q9PDU6	Q9pdu6 streptococc	784	73	6.1	3013	2	Q9QIX9	Q9qix9 hepatitis c
712	73	6.1	255	2	P87639	P87639 equine arte	785	73	6.1	3013	2	Q9QIX0	Q9qix0 hepatitis c
713	73	6.1	255	2	Q9YNU0	Q9ymu0 equine arte	786	73	6.1	6875	2	Q28733	Q28733 oryctolagus
714	73	6.1	261	2	Q7QN39	Q7qn39 anophelis g	787	73	6.1	156	2	Q81516	Q81516 hepatitis c
715	73	6.1	264	2	Q7M552	Q7m552 vibrio vuln	788	73	6.1	156	2	Q81519	Q81519 hepatitis c
716	73	6.1	264	2	Q8DAQ9	Q8daq9 vibrio vuln	789	73	6.1	173	2	Q9WD17	Q9wd17 equine arte
717	73	6.1	279	2	Q6TY95	Q6ty95 xiphinema a	790	73	6.1	174	2	P97065	P97065 salmoneila
718	73	6.1	282	1	NO2M_CABEL	P24889 caenorhabdi	791	73	6.1	180	2	P71252	P71252 escherichia
719	73	6.1	290	2	Q8NX00	Q8nx00 staphylococ	792	73	6.1	180	2	P71254	P71254 escherichia
720	73	6.1	290	2	Q6G9W4	Q6g9w4 staphylococ	793	73	6.1	180	2	P71255	P71255 escherichia
721	73	6.1	295	2	Q8VUQ2	Q8vuq2 pseudomonas	794	73	6.1	180	2	P71256	P71256 escherichia
722	73	6.1	295	2	Q88PN3	Q88pn3 pseudomonas	795	73	6.1	180	2	P71258	P71258 escherichia
723	73	6.1	303	2	Q94EX0	Q94ex0 arabidopsis	796	73	6.1	180	2	P71259	P71259 escherichia
724	73	6.1	314	2	Q8ESH3	Q8esh3 oceanobacil	797	73	6.1	180	2	P71260	P71260 escherichia
725	73	6.1	322	2	Q9H6T9	Q9het9 homo sapien	798	73	6.1	180	2	P71261	P71261 escherichia
726	73	6.1	326	2	Q95NR7	Q95nr7 muscardinus	799	73	6.1	191	2	Q8U4P0	Q8u4p0 pyrococcus
727	73	6.1	335	2	Q85WL8	Q85wl8 encephalito	800	73	6.1	208	2	Q63447	Q63447 echinotrix
728	73	6.1	339	1	SRG7_CABEL	PS4123 caenorhabdi	801	73	6.1	208	2	Q7J7L2	Q7j7l2 echinotrix
729	73	6.1	340	2	Q9N2T2	Q9n2t2 caenorhabdi	802	73	6.1	209	2	Q7J7L0	Q7j7l0 echinotrix
730	73	6.1	343	2	Q7YFUD	Q7yfu0 myrmica bul	803	73	6.1	209	2	Q8GZ10	Q8gz10 arabidopsis
731	73	6.1	343	2	Q85AS7	Q85aet una scopari	804	73	6.1	209	2	Q49834	Q49834 mycobacteri
732	73	6.1	348	2	Q9TD49	Q9td49 cyrtolobias	805	73	6.1	210	2	Q7J7L9	Q7j7l9 echinotrix
733	73	6.1	364	1	GHSR_MOUSE	Q93p50 mus musculu	806	73	6.1	211	2	Q7J7L3	Q7j7l3 echinotrix
734	73	6.1	364	1	GHSR_RAT	Q08725 rattus norv	807	73	6.1	214	2	Q63950	Q63950 echinotrix
735	73	6.1	375	2	Q86NC0	Q86nc0 caenorhabdi	808	73	6.1	217	2	Q9XMK7	Q9xmk7 ochotona pr
736	73	6.1	378	2	Q70BC4	Q70eg4 saccolomus	809	73	6.1	224	2	Q8RGE6	Q8rge6 fusobacteri
737	73	6.1	378	2	Q70EG5	Q70eg5 saccolomus	810	73	6.1	225	2	Q7M2C0	Q7m2c0 leishmania
738	73	6.1	379	1	CYB_CRATU	Q8wdv6 cratogeomys	811	73	6.1	259	2	Q8RES9	Q8res9 fusobacteri
739	73	6.1	379	2	Q8MDV7	Q8mdv7 cratogeomys	812	73	6.1	285	2	Q86DD6	Q86dd6 caenorhabdi
740	73	6.1	379	2	Q34039	Q34039 cratogeomys	813	73	6.1	291	2	Q24561	Q24561 zea mays (m
741	73	6.1	379	2	Q698Q2	Q698q2 cratogeomys	814	73	6.1	298	2	Q8R2A8	Q8r2a8 mus musculu
742	73	6.1	383	2	Q9GL20	Q9gl20 cynopterus	815	73	6.1	308	2	Q6M472	Q6m472 rhodopsendo
743	73	6.1	391	1	Y450_BUCAP	Q8k99 buchneria ap	816	73	6.1	309	2	Q710E1	Q71ue1 bos taurus
744	73	6.1	394	2	Q6EE99	Q6ee99 latimeria c	817	73	6.1	315	2	Q91G02	Q91g02 arabidopsis
745	73	6.1	399	2	Q6LQJ3	Q6lqj3 picophilus	818	73	6.1	320	1	Q9X2_LACIA	Q9xch9 iactococcus
746	73	6.1	401	2	Q6KZX3	Q6kzx3 picophilus	819	73	6.1	325	2	Q9CIT9	Q9cch9 laccococcus
747	73	6.1	446	2	Q8H9B3	Q8h9b3 brassica ca	820	73	6.1	336	2	Q17077	Q17077 caenorhabdi
748	73	6.1	450	1	VELM_EHY1B	P28948 equine herp	821	73	6.1	348	2	Q99924	Q99924 cyprinella
749	73	6.1	450	2	Q6DLF9	Q6dlf9 equid herpe	822	73	6.1	348	2	Q833B9	Q833b9 enterococcu
750	73	6.1	450	2	Q6S6V2	Q6s6v2 equid herpe	823	73	6.1	350	2	Q835L2	Q835l2 enterococcu
751	73	6.1	453	2	Q94307	Q94307 caenorhabdi	824	73	6.1	356	2	Q8FYM4	Q8fym4 bruceila su
752	73	6.1	461	2	Q9R923	Q9r923 streptococc	825	73	6.1	363	2	Q70US3	Q70us3 diflofilaria
753	73	6.1	474	2	Q94C17	Q94c17 arabidopsis	826	73	6.1	363	2	Q6HGU9	Q6hgu9 bacillus th
754	73	6.1	487	2	Q7MBA5	Q7mba5 photorhabdu	827	73	6.1	374	2	Q8MKR0	Q8mkr0 ovis aries
755	73	6.1	494	1	KCF1_HUMAN	Q9h3no homo sapien	828	73	6.1	379	1	CYB_OCHAL	Q9gby1 ochotona al
756	73	6.1	510	2	Q27072	Q27072 taenia soli	829	73	6.1	379	1	CYB_OCHCU	Q9g1b9 ochotona cu
757	73	6.1	553	2	Q9ZJ75	Q9zj75 helicobacte	830	73	6.1	379	1	CYB_OCHHI	Q9gby6 ochotona hi
758	73	6.1	556	2	Q7QZJ9	Q7qzj9 giardia lam	831	73	6.1	379	1	CYB_OCHHY	Q9g6c2 ochotona ny
759	73	6.1	616	2	Q6B1O1	Q6b1o1 debaryomyce	832	73	6.1	379	1	CYB_OCHKO	Q9gdp0 ochotona ko
760	73	6.1	635	2	Q86X77	Q86x77 homo sapien	833	73	6.1	379	1	CYB_OCHNB	Q9gdb2 ochotona nu
761	73	6.1	643	2	Q7NBK6	Q7nbk6 mycoplasma	834	73	6.1	379	1	CYB_OCHRO	Q9gdb5 ochotona ro



835	72.5	6.1	379	1	CYB_OCHRU	092zu1	ochotona ru	908	72	6.0	226	2	Q7TEH2	Q7teh2	avian infec
836	72.5	6.1	379	1	CYB_OCHTH	09gbt6	ochotona th	909	72	6.0	227	2	Q7Y6X7	Q7y6x7	ligriopus c
837	72.5	6.1	379	1	CYB_OCHTI	09gbt7	ochotona th	910	72	6.0	229	2	Q20551	Q20551	urnus amerl
838	72.5	6.1	379	2	Q70UT5	070ut5	ochotona pr	911	72	6.0	249	2	Q8E9R2	Q8e9r2	shewanella
839	72.5	6.1	379	2	Q71IX8	071ix8	ochotona ca	912	72	6.0	254	2	Q812U8	Q812u8	bacillus ce
840	72.5	6.1	379	2	Q85AV3	085av3	chimarogal	913	72	6.0	254	2	Q81MK0	Q81mk0	bacillus an
841	72.5	6.1	379	2	Q9G1C3	09g1c3	ochotona ca	914	72	6.0	276	2	Q9HJV7	Q9hJV7	thermoplasm
842	72.5	6.1	379	2	Q9G1C4	09g1c4	ochotona an	915	72	6.0	279	2	Q9XXT1	Q9xxT1	caenorhabdi
843	72.5	6.1	379	2	Q9GAM7	09gam7	chaetodipus	916	72	6.0	286	2	Q6HK77	Q6hk77	bacillus th
844	72.5	6.1	379	2	Q9GBY2	09gby2	ochotona ca	917	72	6.0	280	2	Q6SHA6	Q6sha6	uncultured
845	72.5	6.1	379	2	Q9GBY8	09gby8	ochotona hu	918	72	6.0	303	2	Q64RZ2	Q64rz2	bacteroides
846	72.5	6.1	379	2	Q9GBZ1	09gbz1	ochotona hy	919	72	6.0	306	2	Q6HWV3	Q6hwv3	bacillus an
847	72.5	6.1	379	2	Q9GBZ1	09gbz1	ochotona la	920	72	6.0	306	2	Q8Y980	Q8y980	listeria mo
848	72.5	6.1	379	2	Q9GBZ3	09gbz3	ochotona pa	921	72	6.0	306	2	Q6ODA2	Q6oda2	leptostreus
849	72.5	6.1	379	2	Q8EWI6	Q8ewi6	mycoplasma	922	72	6.0	311	2	Q8VRF2	Q8vrf2	mus musculu
850	72.5	6.1	387	2	Q6RKP6	Q6rkp6	human harpe	923	72	6.0	317	2	Q9CKI6	Q9cki6	pasteurella
851	72.5	6.1	389	1	OXYR_HUMAN	P30559	homo sapien	924	72	6.0	330	2	Q7ZUC3	Q7zuc3	brachydanio
852	72.5	6.1	402	2	Q8WMQ9	Q8wmq9	ovis aries	925	72	6.0	332	2	Q88TJ9	Q88tj9	lactobacill
853	72.5	6.1	428	2	Q66CP9	Q66cf9	yersinia ps	926	72	6.0	334	2	Q88XJ9	Q88xj9	lactobacill
854	72.5	6.1	428	2	Q8ZG86	Q8zgb6	yersinia pe	927	72	6.0	335	2	Q9ZYJ2	Q9zyJ2	oryzeteropus
855	72.5	6.1	442	2	Q6LOY3	Q6loy3	pietrophilus	928	72	6.0	338	2	Q9XTR2	Q9xtR2	caenorhabdi
856	72.5	6.1	442	2	Q6PHK5	Q6phk5	brachydanio	929	72	6.0	339	2	Q97GD6	Q97gd6	clostridium
857	72.5	6.1	445	2	Q6NYH8	Q6nyh8	brachydanio	930	72	6.0	343	2	Q85AT6	Q85at6	uma scopari
858	72.5	6.1	452	2	Q9T9N6	Q9t9n6	terebratul	931	72	6.0	343	2	Q9BAH5	Q9bah5	uma scopari
859	72.5	6.1	452	2	Q6P8Z2	Q6p8z2	xenopus tro	932	72	6.0	343	2	Q9TD07	Q9td07	rachovia ma
860	72.5	6.1	478	2	Q97OD2	Q97od2	sulfolobus	933	72	6.0	379	1	CYB_GEOP1	Q9tez5	geomya pine
861	72.5	6.1	491	2	Q6SWI8	Q6swi8	human cytom	934	72	6.0	379	1	CYB_THOMA	Q8wek7	thomomys ma
862	72.5	6.1	499	1	WVIN_AQUAE	Q67658	aquilex aeo	935	72	6.0	379	2	Q8W6K4	Q8w6k4	cratogeomys
863	72.5	6.1	505	2	Q8ORV6	Q8ory6	pongine her	936	72	6.0	379	2	Q8WDV3	Q8wdv3	cratogeomys
864	72.5	6.1	513	1	PACR_BOVIN	Q29627	bos taurus	937	72	6.0	379	2	Q698Q3	Q698q3	cratogeomys
865	72.5	6.1	522	2	Q23444	Q23444	caenorhabdi	938	72	6.0	379	2	Q71IO9	Q71io9	cratogeomys
866	72.5	6.1	526	2	Q6FDP6	Q6fdf6	acinetobact	939	72	6.0	379	2	Q9THD6	Q9thd6	oryzeteropus
867	72.5	6.1	538	2	Q7VSL1	Q7vsl1	borderella	940	72	6.0	386	1	CYB_SARGL	Q63848	sarcophyton
868	72.5	6.1	539	2	Q7W4I6	Q7w4i6	borderella	941	72	6.0	391	2	Q8RLY7	Q8rly7	salmonella
869	72.5	6.1	539	2	Q7WFK3	Q7wfk3	borderella	942	72	6.0	391	2	Q8RLY9	Q8rly9	salmonella
870	72.5	6.1	574	2	Q6LH28	Q6lh28	photobacter	943	72	6.0	392	2	Q9LCN9	Q9lcn9	micromonas
871	72.5	6.1	614	2	Q7U5J3	Q7u5j3	synecococc	944	72	6.0	396	1	CYB_LAMPL	Q9tao0	lampetra fl
872	72.5	6.1	635	2	Q21335	Q21335	caenorhabdi	945	72	6.0	415	1	L52_ADE05	P04469	human adeno
873	72.5	6.1	660	2	Q8AW53	Q8aw53	brachydanio	946	72	6.0	415	2	Q6VGJ2	Q6vgj2	human adeno
874	72.5	6.1	661	2	Q6G4Y3	Q6g4y3	bartonella	947	72	6.0	415	2	Q6VGY2	Q6vgy2	human adeno
875	72.5	6.1	662	2	Q6G146	Q6g146	bartonella	948	72	6.0	415	2	Q71BX5	Q71bx5	human adeno
876	72.5	6.1	666	1	RUP_STRA3	Q8575	streptococc	949	72	6.0	415	2	Q7M5Z2	Q7m5z2	human adeno
877	72.5	6.1	671	2	Q6MCR0	Q6mcro	parachlamyd	950	72	6.0	415	2	Q7M6J3	Q7m6j3	human adeno
878	72.5	6.1	686	2	Q8EKS6	Q8ek6	shewanella	951	72	6.0	417	2	Q9NTJ9	Q9ntj9	homo sapien
879	72.5	6.1	686	2	Q9TUT2	Q9tut2	muscula vis	952	72	6.0	418	2	Q6QRB5	Q6qrb5	legionella
880	72.5	6.1	717	2	Q7RICO	Q7ric0	plasmodium	953	72	6.0	418	2	Q6QFC3	Q6qfc3	legionella
881	72.5	6.1	718	2	Q48872	Q48872	lactobacill	954	72	6.0	419	2	Q66IU4	Q66iu4	xenopus tro
882	72.5	6.1	734	2	Q6ZPP2	Q6zpz2	mus musculu	955	72	6.0	444	1	Q6GRK5	Q6grk5	staphylococ
883	72.5	6.1	756	2	Q8C9E3	Q8c9e3	mus musculu	956	72	6.0	448	1	INVX_SCHPO	Q42878	schizosacch
884	72.5	6.1	769	2	Q9N3Y9	Q9n3y9	caenorhabdi	957	72	6.0	448	2	Q460J4	Q460j4	drosophila
885	72.5	6.1	832	2	Q64MT1	Q64mt1	bacteroides	958	72	6.0	453	2	Q99XP2	Q99xp2	staphylococ
886	72.5	6.1	848	2	Q8VZH3	Q8vzh3	arabidopsis	959	72	6.0	453	2	Q7A6D9	Q7a6d9	staphylococ
887	72.5	6.1	848	2	Q9S1U2	Q9s1u2	arabidopsis	960	72	6.0	453	2	Q7NWT7	Q7nwt7	chromobacte
888	72.5	6.1	858	2	Q74I85	Q74i85	lactobacill	961	72	6.0	465	2	Q9RDT2	Q9rdt2	staphylococ
889	72.5	6.1	1103	2	Q753W8	Q753w8	ashbya goss	962	72	6.0	468	2	Q94K50	Q94k50	arabidopsis
890	72.5	6.1	1304	2	Q8MNJ0	Q8mnj0	dictyosteli	963	72	6.0	479	1	COO6_YEAST	P53318	saccharomyc
891	72.5	6.1	1357	2	Q817K7	Q817k7	caenorhabdi	964	72	6.0	497	2	Q9VFS9	Q9vfs9	arabidopsis
892	72.5	6.1	1526	2	Q19611	Q19611	caenorhabdi	965	72	6.0	518	2	Q7VQX6	Q7vqx6	candidatus
893	72.5	6.1	1548	2	Q70409	Q7q409	anopheles g	966	72	6.0	523	2	Q86YB4	Q86yb4	homo sapien
894	72.5	6.1	1689	2	Q8QZP4	Q8qzpz	crimean-con	967	72	6.0	530	2	Q65124	Q65124	african bwi
895	72.5	6.1	1689	2	Q9J1H9	Q9j1h9	crimean-con	968	72	6.0	552	2	Q6NHU7	Q6nhu7	corynebacte
896	72.5	6.1	1702	2	Q95OK2	Q95qk2	caenorhabdi	969	72	6.0	553	2	Q975L9	Q975l9	arabidopsis
897	72.5	6.1	4097	2	Q7RG07	Q7rg07	plasmodium	970	72	6.0	556	2	Q93YN6	Q93yn6	arabidopsis
898	72	6.0	156	2	Q6VXR9	Q6vrx9	helicobacte	971	72	6.0	562	2	Q6CF79	Q6cfr9	yarowia li
899	72	6.0	156	2	Q81540	Q81540	hepatitis c	972	72	6.0	594	2	Q7L8K9	Q7l8k9	homo sapien
900	72	6.0	173	2	Q9WD22	Q9wd22	equine arte	973	72	6.0	596	2	Q8R7C9	Q8r7c9	thermoanaer
901	72	6.0	173	2	Q9WD25	Q9wd25	equine arte	974	72	6.0	600	2	Q429J2	Q429j2	schizosacch
902	72	6.0	182	2	Q988T5	Q988t5	rhizobium 1	975	72	6.0	610	2	Q84EX2	Q84ex2	tetraselmis
903	72	6.0	200	2	Q41199	Q41199	porcine rep	976	72	6.0	630	2	Q24508	Q24508	dianthus ca
904	72	6.0	200	2	Q9J7J6	Q9j7j6	porcine rep	977	72	6.0	632	2	Q8DDJ4	Q8ddj4	xenopus lae
905	72	6.0	209	2	Q85UJ0	Q85uj0	ciona savig	978	72	6.0	636	2	Q957I9	Q957i9	homo sapien
906	72	6.0	225	2	Q6DTU8	Q6dtu8	avian infec	979	72	6.0	636	2	Q9UBH6	Q9ubh6	homo sapien
907	72	6.0	225	2	Q64PZ0	Q64pfz0	avian infec	980	72	6.0	712	2	Q94BK6	Q94ek6	plasm bactiv

981	72	6.0	716	2	Q7N732	Q7N732	photorhabdu	1054	71.5	6.0	379	2	Q698Q0	Q698Q0	cratogeomys
982	72	6.0	721	2	Q671A6	Q671A6	syndiotact	1055	71.5	6.0	379	2	Q71BM1	Q71BM1	glaucomys s
983	72	6.0	736	2	Q7U76	Q7U76	dirosophila	1056	71.5	6.0	379	2	Q9TF66	Q9TF66	peromophilu
984	72	6.0	772	2	Q75JP4	Q75JP4	dictyosteli	1057	71.5	6.0	381	2	Q8ZXP7	Q8ZXP7	pyrobaculum
985	72	6.0	782	2	Q8TD05	Q8TD05	homo sapien	1058	71.5	6.0	381	2	Q79571	Q79571	musculus ma
986	72	6.0	796	2	Q75D67	Q75D67	ababya goos	1059	71.5	6.0	381	2	Q6RKP4	Q6RKP4	human herpe
987	72	6.0	844	2	Q750H3	Q750H3	ababya goos	1060	71.5	6.0	382	2	Q9N7N8	Q9N7N8	human herpe
988	72	6.0	878	2	Q9VSK2	Q9VSK2	dirosophila	1061	71.5	6.0	383	1	Y1V4_SCHPO	Y1V4_SCHPO	schistosach
989	72	6.0	928	2	Q660E1	Q660E1	borrelia ga	1062	71.5	6.0	386	1	QXVR_PIG	QXVR_PIG	sus scrofa
990	72	6.0	1035	2	Q875W8	Q875W8	saccharomyc	1063	71.5	6.0	386	2	Q8R376	Q8R376	thermoanaer
991	72	6.0	1038	1	YKDJ_YEAST	YKDJ_YEAST	saccharomyc	1064	71.5	6.0	388	2	Q8SQ91	Q8SQ91	myceris th
992	72	6.0	1094	1	PDOD_PLAFK	PDOD_PLAFK	saccharomyc	1065	71.5	6.0	388	2	Q8SQ93	Q8SQ93	myceris gr
993	72	6.0	1094	1	PDOD_PLAFK	PDOD_PLAFK	plasmodium	1066	71.5	6.0	390	1	ITR_CARCO	ITR_CARCO	catostomus
994	72	6.0	1113	2	Q9XK4	Q9XK4	caenorhabdi	1067	71.5	6.0	392	2	Q9A8H8	Q9A8H8	streplococc
995	72	6.0	1220	1	PTCI_BRARE	PTCI_BRARE	brachydanio	1068	71.5	6.0	407	2	Q6DG01	Q6DG01	brachydanio
996	72	6.0	1267	2	Q9U0T5	Q9U0T5	leishmania	1069	71.5	6.0	410	2	Q82AH6	Q82AH6	streplococce
997	72	6.0	1275	1	TRP_DROME	TRP_DROME	dirosophila	1070	71.5	6.0	418	2	Q7NKE2	Q7NKE2	gloeobacter
998	72	6.0	1275	1	Q9VAF1	Q9VAF1	dirosophila	1071	71.5	6.0	419	2	Q7VAC4	Q7VAC4	prochlorococ
999	72	6.0	1282	2	Q24809	Q24809	entamoeba h	1072	71.5	6.0	431	2	Q6RH32	Q6RH32	rattus norv
1000	72	6.0	1477	2	Q9C250	Q9C250	neurospora	1073	71.5	6.0	435	2	Q8Y5E0	Q8Y5E0	listeria norv
1001	72	6.0	1513	2	Q7RVU0	Q7RVU0	neurospora	1074	71.5	6.0	435	2	Q929P5	Q929P5	listeria mo
1002	72	6.0	3010	2	Q9QIX1	Q9QIX1	hepatitis c	1075	71.5	6.0	435	2	Q71XN9	Q71XN9	listeria mo
1003	72	6.0	3010	2	Q9QIX2	Q9QIX2	hepatitis c	1076	71.5	6.0	435	2	Q891I7	Q891I7	bradyrhizob
1004	71.5	6.0	161	2	Q88242	Q88242	dennyus som	1077	71.5	6.0	436	2	Q89EQ8	Q89EQ8	bradyrhizob
1005	71.5	6.0	198	2	Q86X19	Q86X19	homo sapien	1078	71.5	6.0	470	2	Q05351	Q05351	entamoeba h
1006	71.5	6.0	210	2	Q8EVE1	Q8EVE1	leptospi	1079	71.5	6.0	486	2	Q62XJ5	Q62XJ5	bacillus 11
1007	71.5	6.0	210	2	Q37682	Q37682	typanoplas	1080	71.5	6.0	489	2	Q65M56	Q65M56	bacillus 11
1008	71.5	6.0	225	1	VME1_IBV6	PM5136	avian infec	1081	71.5	6.0	501	2	Q9XH61	Q9XH61	matricaria
1009	71.5	6.0	227	2	Q9GAT7	Q9GAT7	ochrona co	1082	71.5	6.0	501	2	Q6DB53	Q6DB53	erwinia car
1010	71.5	6.0	229	2	Q7NB29	Q7NB29	mycoplasma	1083	71.5	6.0	510	1	HEX5_RICCO	HEX5_RICCO	ricinus com
1011	71.5	6.0	235	2	Q03191	Q03191	monocorium	1084	71.5	6.0	518	2	Q880G3	Q880G3	pseudomonas
1012	71.5	6.0	237	2	Q06251	Q06251	mycobacteri	1085	71.5	6.0	521	2	Q6CVF0	Q6CVF0	Kluyveromyc
1013	71.5	6.0	237	2	Q7TW15	Q7TW15	mycobacteri	1086	71.5	6.0	524	2	Q80905	Q80905	arabidopsis
1014	71.5	6.0	246	2	Q8YB21	Q8YB21	brucella me	1087	71.5	6.0	524	2	Q6NH85	Q6NH85	corynebacte
1015	71.5	6.0	254	2	Q8LX09	Q8LX09	lammaria d	1088	71.5	6.0	536	2	Q81F50	Q81F50	bacillus ce
1016	71.5	6.0	255	2	Q66480	Q66480	equine arte	1089	71.5	6.0	550	2	Q8VMK1	Q8VMK1	pseudomonas
1017	71.5	6.0	257	2	Q71W44	Q71W44	listeria mo	1090	71.5	6.0	550	2	Q881W5	Q881W5	pseudomonas
1018	71.5	6.0	266	2	Q8XP47	Q8XP47	clostridium	1091	71.5	6.0	603	2	Q99R71	Q99R71	staphylococ
1019	71.5	6.0	270	2	Q8H1Y5	Q8H1Y5	perognathus	1092	71.5	6.0	603	2	Q792Y2	Q792Y2	staphylococ
1020	71.5	6.0	301	2	Q9CJ24	Q9CJ24	lactococcus	1093	71.5	6.0	603	2	Q7A3D6	Q7A3D6	staphylococ
1021	71.5	6.0	314	1	OR3_MOUSE	Q89133	thermoplasma	1094	71.5	6.0	603	2	Q666A7	Q666A7	staphylococ
1022	71.5	6.0	320	2	Q9FAT0	Q9FAT0	vibrio para	1095	71.5	6.0	603	2	Q6GDN2	Q6GDN2	staphylococ
1023	71.5	6.0	326	2	Q7L853	Q7L853	homo sapien	1096	71.5	6.0	651	2	Q9M2X4	Q9M2X4	arabidopsis
1024	71.5	6.0	336	2	Q9BF45	Q9BF45	ceratotheri	1097	71.5	6.0	663	2	Q66RH5	Q66RH5	rattus norv
1025	71.5	6.0	326	2	Q9BF57	Q9BF57	hylobates c	1098	71.5	6.0	669	1	YH06_HAEIN	YH06_HAEIN	haemophilus
1026	71.5	6.0	328	2	Q89R48	Q89R48	bradyrhizob	1099	71.5	6.0	670	1	SI42_RAT	SI42_RAT	rattus norv
1027	71.5	6.0	332	2	Q8GIP3	Q8GIP3	caenorhabdi	1100	71.5	6.0	715	2	Q7Z4M8	Q7Z4M8	homo sapien
1028	71.5	6.0	334	2	Q9TZ00	Q9TZ00	caenorhabdi	1101	71.5	6.0	725	1	MTBR_HUMAN	MTBR_HUMAN	homo sapien
1029	71.5	6.0	336	2	Q79425	Q79425	neomys fodi	1102	71.5	6.0	733	2	Q8GT52	Q8GT52	hordium vul
1030	71.5	6.0	336	2	Q9TH84	Q9TH84	seorex radde	1103	71.5	6.0	814	2	Q8D341	Q8D341	caenorhabdi
1031	71.5	6.0	336	2	Q800E8	Q800E8	tetradodon n	1104	71.5	6.0	838	2	Q8BD40	Q8BD40	vibrio vuln
1032	71.5	6.0	338	2	Q800D2	Q800D2	tetradodon n	1105	71.5	6.0	858	2	Q661Y5	Q661Y5	dictyosteli
1033	71.5	6.0	339	2	Q8RD25	Q8RD25	thermoanaer	1106	71.5	6.0	890	1	WFS1_HUMAN	WFS1_HUMAN	homo sapien
1034	71.5	6.0	341	2	Q9BR21	Q9BR21	guillardi	1107	71.5	6.0	1407	1	CYAA_DICDI	CYAA_DICDI	dictyosteli
1035	71.5	6.0	342	1	V674_HHY8	Q98146	human herpe	1108	71.5	6.0	1509	2	Q6RCS2	Q6RCS2	ciona bavi
1036	71.5	6.0	342	1	Q90387	Q90387	human herpe	1109	71.5	6.0	1837	2	Q6X3J2	Q6X3J2	pseudomonas
1037	71.5	6.0	348	1	RMFD_VIBCH	Q9K189	vibrio chol	1110	71.5	6.0	2923	1	CLR2_HUMAN	CLR2_HUMAN	pyrococcus
1038	71.5	6.0	348	1	Q999Z2	Q999Z2	cyprinella	1111	71.5	6.0	3010	2	Q68949	Q68949	equine arte
1039	71.5	6.0	355	2	Q8YDX2	Q8YDX2	cellulosa me	1112	71.5	6.0	3589	2	Q6LRF3	Q6LRF3	hepatitis c
1040	71.5	6.0	360	2	Q8H1B6	Q8H1B6	calloscleru	1113	71.5	6.0	5303	2	Q9V628	Q9V628	plasmodium
1041	71.5	6.0	362	2	Q85CY4	Q85CY4	bacillus 11	1114	71.5	6.0	114	2	Q25269	Q25269	helicobacte
1042	71.5	6.0	362	1	Q6PDP2	Q6PDP2	mus musculu	1115	71.5	6.0	150	2	Q82ZC0	Q82ZC0	enterococcu
1043	71.5	6.0	366	1	ML1A_SHEEP	Q84040	ovis aries	1116	71.5	6.0	171	2	Q8U3Q3	Q8U3Q3	pyrococcus
1044	71.5	6.0	369	2	Q70VH8	Q70VH8	seorex minut	1117	71.5	6.0	188	1	SH2A_CANFA	SH2A_CANFA	equine arte
1045	71.5	6.0	375	2	Q6RKP7	Q6RKP7	human herpe	1118	71.5	6.0	188	1	Q9WD21	Q9WD21	canis fami
1046	71.5	6.0	379	1	Q9B_OCHCO	Q9B_OCHCO	ochrona co	1119	71.5	6.0	195	2	Q6MTK4	Q6MTK4	mycoplasma
1047	71.5	6.0	379	1	Q9B_OCHFO	Q9B_OCHFO	ochrona fo	1120	71.5	6.0	199	2	Q8THM3	Q8THM3	methanosa
1048	71.5	6.0	379	1	Q9B_SORR	Q9B_SORR	seorex radde	1121	71.5	6.0	200	2	Q85U08	Q85U08	ceratobaeus
1049	71.5	6.0	379	1	CYB_SPERA	Q9TF55	peromophilu	1122	71.5	6.0	219	2	Q9J7J9	Q9J7J9	porcine rep
1050	71.5	6.0	379	2	Q48007	Q48007	peromophilu	1123	71.5	6.0	223	2	Q931D2	Q931D2	staphylococ
1051	71.5	6.0	379	2	Q8WEK3	Q8WEK3	thomomys ta	1124	71.5	6.0	223	2	Q91NKS	Q91NKS	avian infec
1052	71.5	6.0	379	2	Q952R3	Q952R3	thomomys ta	1125	71.5	6.0	223	2	Q91NKS	Q91NKS	avian infec
1053	71.5	6.0	379	2	Q34661	Q34661	glaucomys b	1126	71.5	6.0	223	2	Q91S95	Q91S95	avian infec

1127	71	5.9	223	2	091596	091596 avian infec	1200	71	5.9	470	1	5H2A_PIG	P50129 sus scrofa
1128	71	5.9	223	1	0915A3	0915A3 avian infec	1201	71	5.9	471	1	5H2A_HUMAN	P28123 homo sapien
1129	71	5.9	225	1	0915A3	P12649 avian infec	1201	71	5.9	472	2	06K136	P68136 mycoplasma
1130	71	5.9	225	2	06R4P1	06R4P1 avian infec	1203	71	5.9	480	2	073CA7	073CA7 bacillus ce
1131	71	5.9	225	2	07TEG9	07TEG9 avian infec	1204	71	5.9	485	2	09CLJ7	09CLJ7 pasteurilla
1132	71	5.9	226	2	07T4O5	07T4O5 avian infec	1205	71	5.9	489	2	08SHRO	08SHRO trichoderma
1133	71	5.9	234	2	09F6V0	09F6V0 bacteroides	1206	71	5.9	492	2	07N9D9	07N9D9 photorhabdu
1134	71	5.9	238	1	09F6V0	081W5 bacillus an	1207	71	5.9	545	1	SOA1_RAT	070556 ratus norv
1135	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1208	71	5.9	546	1	MUP3_YEAST	P38734 saccharomyc
1136	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1209	71	5.9	546	1	0813H5	0813H5 phlebotom
1137	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1210	71	5.9	548	2	08AUN9	08AUN9 fugu rubrip
1138	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1211	71	5.9	554	2	YAS8_SCHPO	010144 schizosacch
1139	71	5.9	242	2	0639U8	0639U8 bacillus ce	1212	71	5.9	563	1	S229_MOUSE	09W16 mus musculu
1140	71	5.9	243	2	034969	034969 myrmecia ba	1213	71	5.9	564	1	06F1V1	06F1V1 mesoplasma
1141	71	5.9	244	2	074HS0	074HS0 lactobacilli	1214	71	5.9	564	1	OCRT1_CABEL	09U539 caenorhabd1
1142	71	5.9	250	2	09KVO3	09KVO3 vibrio chol	1215	71	5.9	564	1	LYTS_STRAU	053705 staphylococ
1143	71	5.9	255	2	066484	066484 equine arte	1216	71	5.9	615	2	07R9S0	07R9S0 plasmodium
1144	71	5.9	258	2	09PP98	09PP98 campylobact	1217	71	5.9	620	2	092ZP7	092ZP7 cyanidlosch
1145	71	5.9	266	2	06W249	06W249 rhizobium s	1218	71	5.9	631	2	081W20	081W20 homo sapien
1146	71	5.9	277	2	070NM1	070NM1 strongyloid	1219	71	5.9	672	2	0650E2	0650E2 bacteroides
1147	71	5.9	279	2	07NEM0	07NEM0 mycoplasma	1220	71	5.9	676	2	004521	004521 arabisdopsis
1148	71	5.9	281	2	08SK19	08SK19 necator ame	1221	71	5.9	701	2	08MWL9	08MWL9 mycoplasma
1149	71	5.9	286	2	063CT1	063CT1 bacillus ce	1222	71	5.9	762	2	08ML23	08ML23 drosophila
1150	71	5.9	289	2	08HZF2	08HZF2 macaca sp.	1223	71	5.9	788	2	092JYB7	092JYB7 helicobacte
1151	71	5.9	290	1	CB4A_ARATH	007473 arabidopsis	1224	71	5.9	826	2	08TOX6	08TOX6 methanosarc
1152	71	5.9	295	2	08P0V2	08P0V2 streptococc	1225	71	5.9	885	2	075SR1	075SR1 ashbya goss
1153	71	5.9	295	2	099ZG3	099ZG3 streptococc	1226	71	5.9	913	2	013099	013099 xenopus lae
1154	71	5.9	308	1	07CNV1	07CNV1 streptococc	1227	71	5.9	913	2	06DDC0	06DDC0 xenopus lae
1155	71	5.9	308	1	SRV1_CABEL	P46564 caenorhabd1	1228	71	5.9	964	2	07SCL0	07SCL0 neurospora
1156	71	5.9	310	1	Y160_BUCAP	08K944 buchnera ap	1229	71	5.9	1021	2	065QR6	065QR6 manihelma
1157	71	5.9	325	2	099NR9	099NR9 tamias stri	1230	71	5.9	1239	2	06CBA1	06CBA1 yarrowia 11
1158	71	5.9	343	2	07YFU4	07YFU4 myrmica kar	1231	71	5.9	1242	2	07T9B1	07T9B1 human cytom
1159	71	5.9	345	2	078911	078911 anolis occu	1232	71	5.9	1409	2	07XW92	07XW92 cryza sattiv
1160	71	5.9	361	2	098P01	098P01 mycoplasma	1233	71	5.9	2304	2	09BMQ4	09BMQ4 bacterella g
1161	71	5.9	374	2	071E55	071E55 galierella s	1234	71	5.9	2423	2	077393	077393 plasmodium
1162	71	5.9	379	1	CYB_CRATY	08Wd1 cratogeomys	1235	71	5.9	2681	2	095V80	095V80 strongyloce
1163	71	5.9	379	1	CYB_THOUM	047993 thomomys um	1236	71	5.9	3010	2	068285	068285 hepaticis c
1164	71	5.9	379	2	047579	047579 thomomys bo	1237	71	5.9	3010	2	081541	081541 hepaticis c
1165	71	5.9	379	2	047981	047981 thomomys bo	1238	71	5.9	3010	2	081825	081825 hepaticis c
1166	71	5.9	379	2	08W7H1	08W7H1 thomomys ma	1239	71	5.9	3010	2	09D7E5	09D7E5 hepaticis c
1167	71	5.9	379	2	0698P7	0698P7 cratogeomys	1240	71	5.9	145	2	065G39	065G39 bacillus 11
1168	71	5.9	379	2	0698P9	0698P9 cratogeomys	1241	71	5.9	203	1	BCRC_BACLI	P42334 bacillus 11
1169	71	5.9	379	2	06OK63	06OK63 ursus thibe	1242	71	5.9	206	2	072LX2	072LX2 leprospira
1170	71	5.9	379	2	09TF00	09TF00 geomys bure	1243	71	5.9	208	2	06BHH0	06BHH0 debratymyce
1171	71	5.9	379	2	09TF03	09TF03 geomys bure	1244	71	5.9	213	2	098E85	098E85 rhizobium 1
1172	71	5.9	380	2	003396	003397 acornys sp.	1245	71	5.9	214	2	066K20	066K20 staphylococ
1173	71	5.9	380	2	003397	06E317 thomomys bo	1246	71	5.9	216	2	06VRP1	06VRP1 helicobacte
1174	71	5.9	380	2	06E3J7	09T502 geomys brev	1247	71	5.9	226	2	003371	003371 dipodomys o
1175	71	5.9	380	2	09T502	09T502 geomys brev	1248	71	5.9	235	2	06BAU8	06BAU8 ovis aries
1176	71	5.9	380	2	09T576	09T576 acornys sp.	1249	71	5.9	235	2	06DHQ1	06DHQ1 brachydanio
1177	71	5.9	380	2	09T577	09T577 acornys sp.	1250	71	5.9	266	2	074888	074888 schizosacch
1178	71	5.9	380	2	09T577	08EMJ1 oceanobacil	1251	71	5.9	266	2	08U854	08U854 agrobacteri
1179	71	5.9	381	1	CYB_PHACT	035409 phascogale	1252	71	5.9	278	2	08SHQ3	08SHQ3 cooperia on
1180	71	5.9	391	2	08RLY8	08RLY8 salmonella	1253	71	5.9	279	2	08YVW2	08YVW2 anabaena sp
1181	71	5.9	391	2	08RSP4	08RSP4 salmonella	1254	71	5.9	283	2	09AKZ0	09AKZ0 lactobacill
1182	71	5.9	391	2	09CGL8	09CGL8 lactococcus	1255	71	5.9	285	2	07S2B8	07S2B8 neurospora
1183	71	5.9	401	2	08S0S5	08S0S5 cryza sattiv	1256	71	5.9	280	2	06SCH2	06SCH2 uncultured
1184	71	5.9	403	2	08ZPR2	08ZPR2 salmonella	1257	71	5.9	291	2	037789	037789 hellanthus
1185	71	5.9	409	2	08ZPR2	09F126 streptomyc	1258	71	5.9	292	2	0746W1	0746W1 geobacter s
1186	71	5.9	416	2	09ABC8	09ABC8 caulobacter	1259	71	5.9	310	2	065VD8	065VD8 manihelma
1187	71	5.9	418	2	06OPB6	06OPB6 legionella	1260	71	5.9	312	2	06CEC0	06CEC0 yarrowia 11
1188	71	5.9	418	2	06OPC0	06OPC0 legionella	1261	71	5.9	315	2	09JRK5	09JRK5 ratus norv
1189	71	5.9	418	2	06OPC1	06OPC1 legionella	1262	71	5.9	320	2	07N0S0	07N0S0 photorhabdu
1190	71	5.9	418	2	06OPC2	06OPC2 legionella	1263	71	5.9	326	2	09B7S9	09B7S9 mania penta
1191	71	5.9	418	2	06OPC4	06OPC4 legionella	1264	71	5.9	326	2	09B7S8	09B7S8 macaca mula
1192	71	5.9	418	2	06OPC6	06OPC6 legionella	1265	71	5.9	335	2	09ZV31	09ZV31 elephanticu
1193	71	5.9	419	2	095081	095081 caenorhabd1	1266	71	5.9	336	2	09THB3	09THB3 sorex pacif
1194	71	5.9	423	2	08Y5H6	08Y5H6 listeria mo	1267	71	5.9	339	2	07PB28	07PB28 rickettsia
1195	71	5.9	428	2	0615Y4	0615Y4 cryza sattiv	1268	71	5.9	340	2	055532	055532 synchocyst
1196	71	5.9	442	2	096ZK3	096ZK3 sulfolobus	1269	71	5.9	343	2	0717B1	0717B1 myrmica nit
1197	71	5.9	448	2	P916B3	P916B3 diptophila	1270	71	5.9	343	2	0717B5	0717B5 myrmica sab
1198	71	5.9	451	2	09SNW3	09SNW3 vernicia fo	1271	71	5.9	343	2	07YFUS	07YFUS myrmica hel
1199	71	5.9	451	2	09F992	09F992 buchnera ap	1272	71	5.9	350	2	09Y370	09Y370 homo sapien

1273	70.5	5.9	351	2	097774	097774 felis silve	1346	70.5	5.9	676	2	Q7RNV6	Q7rnv6 plasmodium
1274	70.5	5.9	352	2	Q98R08	Q98r08 mycoplasma	1347	70.5	5.9	679	2	Q7Q645	Q7q645 anopheles g
1275	70.5	5.9	353	2	Q7TN44	Q7tn44 ractus norv	1348	70.5	5.9	683	2	Q972H7	Q972h7 anophelobus
1276	70.5	5.9	356	2	Q9GC99	Q9gc99 glaucomyx v	1349	70.5	5.9	689	2	Q72YU0	Q72yu0 bacillus ce
1277	70.5	5.9	360	2	Q8HIB8	Q8hib8 callosciuru	1350	70.5	5.9	700	2	Q9LD70	Q9ld70 arabdopsis
1278	70.5	5.9	360	2	Q8HIC3	Q8hic3 callosciuru	1351	70.5	5.9	717	2	Q6NHL8	Q6nhl8 corynebacte
1279	70.5	5.9	361	2	Q9N4V8	Q9n4v8 caenorhabd	1352	70.5	5.9	729	2	Q8ESC5	Q8esc5 oceanobacil
1280	70.5	5.9	363	2	Q9K337	Q9k337 bacillus ce	1353	70.5	5.9	740	2	Q7XCM9	Q7xcm9 oryza sativ
1281	70.5	5.9	363	2	Q7BYCO	Q7byco bacillus ce	1354	70.5	5.9	740	2	Q9FRK0	Q9frk0 oryza sativ
1282	70.5	5.9	366	2	Q6TTN3	Q6ttn3 homo sapien	1355	70.5	5.9	766	2	Q9LZ30	Q9lzt30 arabdopsis
1283	70.5	5.9	369	2	Q70VB2	Q70vb2 seorex volnu	1356	70.5	5.9	769	2	Q7W1T5	Q7w1t5 bordetella
1284	70.5	5.9	370	2	Q6VPS4	Q6vps4 canis famli	1357	70.5	5.9	776	1	CHS1_CANAL	P2336 candida alb
1285	70.5	5.9	370	2	Q7RF50	Q7rf50 plasmodium	1358	70.5	5.9	856	2	Q9FHV2	Q9fhv2 arabdopsis
1286	70.5	5.9	373	2	Q6UJ34	Q6uj34 heptathela	1359	70.5	5.9	859	2	Q9FFI4	Q9ffi4 arabdopsis
1287	70.5	5.9	379	1	CYB_GIAVO	Q6f34 glaucomyx v	1360	70.5	5.9	951	2	Q6PK21	Q6fk21 candida gla
1288	70.5	5.9	379	2	Q48009	Q48009 dipodomys a	1361	70.5	5.9	980	2	Q8A3J1	Q8a3j1 bacteroides
1289	70.5	5.9	379	2	Q48364	Q48364 thionomys bo	1362	70.5	5.9	1026	2	Q9URM1	Q9urm1 candida alb
1290	70.5	5.9	379	2	Q8LM04	Q8lm04 macroscelid	1363	70.5	5.9	1199	2	Q9Y4J9	Q9y4j9 homo sapien
1291	70.5	5.9	379	2	Q8W9L6	Q8w9l6 glaucomyx v	1364	70.5	5.9	1234	2	Q8VDJ4	Q8vdj4 mus musculu
1292	70.5	5.9	379	2	Q85RV3	Q85rv3 muntiacus c	1365	70.5	5.9	1234	2	Q6B4R6	Q6b4r6 mus musculu
1293	70.5	5.9	379	2	Q9GAV5	Q9gav5 dipodomys s	1366	70.5	5.9	1491	2	Q7S5P1	Q7s5p1 neurospora
1294	70.5	5.9	379	2	Q9GAV6	Q9gav6 dipodomys s	1367	70.5	5.9	1583	2	Q92GE9	Q92ge9 rickettsia
1295	70.5	5.9	379	2	Q9GAV7	Q9gav7 dipodomys o	1368	70.5	5.9	1678	2	Q6BD82	Q6bd82 homo sapien
1296	70.5	5.9	379	2	Q9GAV9	Q9gav9 dipodomys e	1369	70.5	5.9	1764	2	Q8BRJ3	Q8brj3 strongyloce
1297	70.5	5.9	379	2	Q9GAN1	Q9gan1 dipodomys e	1370	70.5	5.9	1781	1	AK12_HUMAN	Q02932 homo sapien
1298	70.5	5.9	379	2	Q9GAW5	Q9gaw5 dipodomys s	1371	70.5	5.9	1787	1	CHD3_CAEEL	Q22516 caenorhabd
1299	70.5	5.9	379	2	Q9GBY3	Q9gbv3 ochotona da	1372	70.5	5.9	5138	2	Q9ZW94	Q9zw94 arabdopsis
1300	70.5	5.9	379	2	Q9TEZ7	Q9tez7 geomyx burs	1373	70.5	5.9	80	2	Q7N019	Q7n019 photorhabdu
1301	70.5	5.9	382	2	Q9HIT9	Q9hit9 thermoplasa	1374	70.5	5.9	114	2	Q6VRH8	Q6vrh8 helicobacte
1302	70.5	5.9	386	2	Q6RKP3	Q6rkp3 human herpe	1375	70.5	5.9	114	2	Q7SXL6	Q7sxl6 helicobacte
1303	70.5	5.9	387	1	T2C_PARTIE	Q6rkp3 human herpe	1376	70.5	5.9	146	2	Q8T098	Q8t098 drosophila
1304	70.5	5.9	389	1	MTR_BUFA	Q77181 paramecium	1377	70.5	5.9	154	1	ML1A_PIG	Q02781 sus scrofa
1305	70.5	5.9	390	1	PE23_HUMAN	Q90252 bufo marinu	1378	70.5	5.9	161	2	Q65W32	Q65j32 bacillus li
1306	70.5	5.9	393	2	Q00336	PA3115 homo sapien	1379	70.5	5.9	173	2	Q67EWS	Q67ews equine arte
1307	70.5	5.9	402	2	Q8XIV7	Q00326 homo sapien	1380	70.5	5.9	173	2	Q9WD20	Q9wd20 equine arte
1308	70.5	5.9	404	2	Q00325	Q8xlv7 coriolus ve	1381	70.5	5.9	173	2	Q9WD23	Q9wd23 equine arte
1309	70.5	5.9	403	2	Q9KGT1	Q00325 homo sapien	1382	70.5	5.9	173	2	Q9WD35	Q9wd35 equine arte
1310	70.5	5.9	416	2	Q6Z9G4	Q9kgt1 mycoplasma	1383	70.5	5.9	175	2	Q9HL28	Q9hl28 thermoplasa
1311	70.5	5.9	416	2	Q6VPS5	Q6z9g4 otyza sativ	1384	70.5	5.9	185	2	Q8LAL4	Q8lal4 arabdopsis
1312	70.5	5.9	420	2	Q7BR79	Q6vps5 canis famli	1385	70.5	5.9	189	1	PSBY_ARATH	Q49347 arabdopsis
1313	70.5	5.9	420	2	Q58964	Q7br79 aeromonas p	1386	70.5	5.9	195	2	Q6FRF5	Q6ff5 schistosoma
1314	70.5	5.9	424	2	Q7VP09	Q58964 pyrococcus	1387	70.5	5.9	195	2	Q8SQZ5	Q8sqz5 lepus europ
1315	70.5	5.9	436	2	Q6BUT5	Q7vp09 helicobacte	1388	70.5	5.9	199	1	PSBY_SPTOL	P80470 spiraciola ol
1316	70.5	5.9	440	1	CAPE_STRAU	Q6but5 debaryomyce	1389	70.5	5.9	213	2	Q9LNR6	Q9lnr6 arabdopsis
1317	70.5	5.9	452	2	Q83C47	P39854 staphylococ	1390	70.5	5.9	221	2	Q9B9P3	Q9b9p3 viverra zib
1318	70.5	5.9	460	2	Q7VIR8	Q83c47 coxiella bu	1391	70.5	5.9	223	2	Q9INK4	Q9ink4 avian infec
1319	70.5	5.9	470	2	Q6SED7	Q7vir8 helicobacte	1392	70.5	5.9	224	2	Q8VSW5	Q8vsw5 staphylococ
1320	70.5	5.9	470	2	Q6SPR0	Q6sed7 lactobacill	1393	70.5	5.9	225	1	VMEI_IBVD1	Q9146 avian infec
1321	70.5	5.9	472	2	Q9LCN5	Q6spq0 lactobacill	1394	70.5	5.9	225	1	VMEI_IBVDE	Q9j3h8 avian infec
1322	70.5	5.9	496	2	Q8YCO7	Q9lcn5 micromonosp	1395	70.5	5.9	225	2	Q6VUR1	Q6vur1 avian infec
1323	70.5	5.9	496	2	Q25600	Q8yc07 bruceella me	1396	70.5	5.9	225	2	Q6VUR2	Q6vur2 avian infec
1324	70.5	5.9	496	2	Q8C604	Q25600 helicobacte	1397	70.5	5.9	225	2	Q6W9D6	Q6w9d6 avian infec
1325	70.5	5.9	500	2	Q8ECQ1	Q8c604 staphylococ	1398	70.5	5.9	225	2	Q7TEH1	Q7teh1 avian infec
1326	70.5	5.9	508	2	Q7RQ76	Q8eqq1 oceanobacil	1399	70.5	5.9	225	2	Q7TEH1	Q7teh1 fuesobacteri
1327	70.5	5.9	521	1	CYOA_HABIN	Q7rq76 plasmodium	1400	70.5	5.9	236	2	Q9XMR1	Q9xmr1 phlebotomus
1328	70.5	5.9	536	1	WIN_CHILMU	PA5021 haemophilus	1401	70.5	5.9	238	2	Q6XMR1	Q6xmr1 chromobacte
1329	70.5	5.9	556	2	Q22109	Q9pjb9 chlamydia m	1402	70.5	5.9	249	2	Q6TZAI	Q6tza1 polythachis
1330	70.5	5.9	556	2	Q7VH12	Q22109 caenorhabd	1403	70.5	5.9	253	2	Q7NTR1	Q7ntr1 chromobacte
1331	70.5	5.9	558	2	Q6EICS	Q7vhi2 helicobacte	1404	70.5	5.9	255	2	Q995W3	Q995w3 equine arte
1332	70.5	5.9	574	1	RFT1_YEAST	Q6eics perkinsus m	1405	70.5	5.9	255	2	Q9QKE1	Q9qke1 equine arte
1333	70.5	5.9	585	2	Q7RIV4	P38206 baccharomyc	1406	70.5	5.9	256	2	Q76B99	Q76b99 drosophila
1334	70.5	5.9	598	1	S6A1_MUSCO	Q7riv4 giardia lam	1407	70.5	5.9	257	2	Q6VGA1	Q6vga1 manhelmita
1335	70.5	5.9	599	1	S6A1_MOUSE	PA1648 mus musculu	1408	70.5	5.9	281	2	Q876G0	Q876g0 saccharomyc
1336	70.5	5.9	599	1	S6A1_RAT	P31648 mus musculu	1409	70.5	5.9	281	2	Q7Q0Q29	Q70q0q29 necator ame
1337	70.5	5.9	599	1	S6A1_RAT	P31648 mus musculu	1410	70.5	5.9	287	1	CB4B_ARATH	Q9xf88 arabdopsis
1338	70.5	5.9	633	2	Q7Q8Q2	Q8n4r8 homo sapien	1411	70.5	5.9	289	2	Q8HZF4	Q8hzf4 gorilla gor
1339	70.5	5.9	641	2	Q7PMH7	Q7q8q2 giardia lam	1412	70.5	5.9	289	2	Q8HZF5	Q8hzf5 pan troglod
1340	70.5	5.9	658	2	Q7ZDUF5	Q7pmh7 anopheles g	1413	70.5	5.9	289	2	Q7NIV8	Q7niv8 gloeobacter
1341	70.5	5.9	662	1	T9S2_MOUSE	Q7zufs brachydanio	1414	70.5	5.9	292	1	ATP6_MYCGR	P47645 mycoplasma
1342	70.5	5.9	662	1	T9S2_MOUSE	P58021 mus musculu	1415	70.5	5.9	292	2	Q92KZ8	Q92kz8 rhizobiolum m
1343	70.5	5.9	662	2	Q8CFP9	Q8c614 mus musculu	1416	70.5	5.9	295	2	Q6SURI	Q6sur1 manhelmita
1344	70.5	5.9	667	2	Q8G6F4	Q8cfp9 mus musculu	1417	70.5	5.9	299	2	Q6MGO9	Q6mog9 methanococ
1345	70.5	5.9	676	2	Q7Q114	Q8g6f4 malawimonas	1418	70.5	5.9	302	2	Q9M7X8	Q9m7x8 arabdopsis
						Q7q114 anopheles g							

1419	70	5.9	303	2	08KJ79	08KJ79 rhizobium 1
1420	70	5.9	305	2	087R04	087R04 vibrio para
1421	70	5.9	307	2	097T64	097T64 streptococ
1422	70	5.9	307	2	08DRJ7	08DRJ7 streptococ
1423	70	5.9	308	2	06FSR9	06FSR9 candida gla
1424	70	5.9	311	2	09JHE2	09JHE2 rattus norv
1425	70	5.9	325	2	09G3Z5	09G3Z5 lithobius f
1426	70	5.9	328	2	08D0N5	08D0N5 yerarsinia pe
1427	70	5.9	330	2	094303	094303 caenorhabdi
1428	70	5.9	332	2	08SEB3	08SEB3 mtu tubero
1429	70	5.9	333	1	08P8_HUMAN	08P8_HUMAN
1430	70	5.9	333	2	06NM05	06NM05 homo sapien
1431	70	5.9	333	2	06NM06	06NM06 homo sapien
1432	70	5.9	345	2	06X0B8	06X0B8 anolis whit
1433	70	5.9	345	2	06X0B8	06X0B8 anolis whit
1434	70	5.9	345	2	06X0C1	06X0C1 anolis whit
1435	70	5.9	345	2	06X0C4	06X0C4 anolis whit
1436	70	5.9	353	2	08TNU4	08TNU4 methanocarc
1437	70	5.9	365	2	09XMT1	09XMT1 tetrahymena
1438	70	5.9	365	2	06A7G0	06A7G0 propionibac
1439	70	5.9	371	2	09NT82	09NT82 homo sapien
1440	70	5.9	378	2	06UVN5	06UVN5 toxodonta c
1441	70	5.9	378	2	071FH4	071FH4 mungocitlis
1442	70	5.9	379	1	CYB_SORTU	079464 seorex tundr
1443	70	5.9	379	1	CYB_ZIPCA	036262 ziphius cav
1444	70	5.9	379	2	047578	047578 thomomys bo
1445	70	5.9	379	2	047583	047583 thomomys bo
1446	70	5.9	379	2	047994	047994 thomomys um
1447	70	5.9	379	2	08LVE7	08LVE7 proteles cr
1448	70	5.9	379	2	08LMD6	08LMD6 parahaena
1449	70	5.9	379	2	08W935	08W935 thomomys ma
1450	70	5.9	379	2	08WDU4	08WDU4 cratogeomys
1451	70	5.9	379	2	08WEK4	08WEK4 thomomys ta
1452	70	5.9	379	2	034837	034837 kogia salmus
1453	70	5.9	379	2	06TL84	06TL84 geomya texe
1454	70	5.9	379	2	071FH8	071FH8 nandinia bl
1455	70	5.9	379	2	07Y8J5	07Y8J5 procavia ca
1456	70	5.9	379	2	08HB13	08HB13 thomomys bo
1457	70	5.9	379	2	08HB66	08HB66 thomomys bo
1458	70	5.9	379	2	08HB83	08HB83 thomomys bo
1459	70	5.9	379	2	08HBK4	08HBK4 thomomys bo
1460	70	5.9	379	2	08HHJ3	08HHJ3 thomomys bo
1461	70	5.9	379	2	08HHJ5	08HHJ5 thomomys bo
1462	70	5.9	379	2	08HHJ6	08HHJ6 thomomys bo
1463	70	5.9	379	2	08HH08	08HH08 thomomys bo
1464	70	5.9	380	2	06E3J6	06E3J6 thomomys bo
1465	70	5.9	381	1	CYB_DASAL	034289 dasyurus al
1466	70	5.9	381	1	CYB_DASNA	034321 dasyurus ha
1467	70	5.9	381	1	CYB_DASSP	034339 dasyurus sp
1468	70	5.9	381	1	CYB_DASTI	034339 dasyurus vi
1469	70	5.9	381	1	CYB_MYOME	035038 myoictis me
1470	70	5.9	381	1	CYB_MYOMA	020603 myoictis wa
1471	70	5.9	388	1	OXYR_MOUSE	P97926 mus musculu
1472	70	5.9	388	1	OXYR_RAT	P70536 rattus norv
1473	70	5.9	388	2	08R5E1	08R5E1 rattus norv
1474	70	5.9	399	2	096A40	096A40 homo sapien
1475	70	5.9	399	2	08MIDO	08MIDO manis tatra
1476	70	5.9	407	2	086894	086894 streptococ
1477	70	5.9	407	2	09RIN7	09RIN7 streptococ
1478	70	5.9	416	2	09MON4	09MON4 arabiidopsi
1479	70	5.9	418	2	054543	054543 legioneila
1480	70	5.9	418	2	06QFB3	06QFB3 legioneila
1481	70	5.9	420	2	09WZ65	09WZ65 thermotoga
1482	70	5.9	420	2	082490	082490 arabiidopsi
1483	70	5.9	427	2	06MDN6	06MDN6 parachlamyd
1484	70	5.9	427	2	08X561	08X561 escherichia
1485	70	5.9	437	2	08FAV1	08FAV1 escherichia
1486	70	5.9	437	2	083P88	083P88 shigella fl
1487	70	5.9	438	2	08UDM3	08UDM3 agrobacteri
1488	70	5.9	450	2	039292	039292 equid herpe
1489	70	5.9	452	2	07RNL9	07RNL9 plasmodium
1490	70	5.9	461	2	07N4W5	07N4W5 photorhabdu
1491	70	5.9	467	2	06CTW7	06CTW7 yarrowia ll

1492	70	5.9	467	2	08MPH2	08MPH2 trypanosoma
1493	70	5.9	476	2	06A0F5	06A0F5 desulfocale
1494	70	5.9	479	2	087J34	087J34 vibrio chol
1495	70	5.9	494	2	023508	023508 caenorhabdi
1496	70	5.9	494	2	08NXW6	08NXW6 staphylococ
1497	70	5.9	494	2	099W27	099W27 staphylococ
1498	70	5.9	494	2	07A762	07A762 staphylococ
1499	70	5.9	494	2	06GBO3	06GBO3 staphylococ
1500	70	5.9	494	2	06G3B5	06G3B5 staphylococ

  

ALIGNMENTS					
RESULT 1	MENT_HUMAN	STANDARD;	PRT;	234 AA.	
AC	095772;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	MUN64 N-terminal domain homolog (STARD3 N-terminal like protein) (UNQ0855/PRO1864).				
DE	Name=STARD3NL; Synonyms=MENTHO;				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A., CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND ALTERNATIVE INITIATION.				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=2287296; PubMed=1293907; DOI=10.1074/jbc.M208290200;				
RT	Alpy F., Wendling C., Rio M.-C., Tomasello C.;				
RL	"MENTHO, a MUN64 homologue devoid of the STARD domain.";				
RN	J. Biol. Chem. 277:50780-50787(2002).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;				
RT	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heidens S., Hang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A., Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";				
RL	Genome Res. 13:2265-2270(2003).				
RP	SEQUENCE FROM N.A.				
RA	Arnett C., Wohldmann P., Le T.;				
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain, and Kidney;				
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603699;				
RT	Straussberg R.L., Felingold E.A., Grouse L.H., Derje J.G.,				
RL	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F., Diatzenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toohilyuk S., Cammick P., Prange C., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiy S.W., Villalano D.K., Muzny D.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Halton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal  
 CC membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, 1 (shown here) and 2, are produced by  
 CC alternative initiation;  
 CC -1- PTM: Phosphorylated.  
 CC -1- SIMILARITY: Contains 1 MENTAL domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC -----  
 CC EMBL: AJ92267; CAB37353.1; -  
 CC DR EMBL: AY358645; AA089008.1; -  
 CC DR EMBL: AC006033; AA07552.1; -  
 CC DR EMBL: BC003074; AA03074.1; -  
 CC DR EMBL: BC005959; AA005959.1; -  
 CC DR Genew; HGNC:19169; STAND3L.  
 CC KW Alternative initiation; Phosphorylation; Transmembrane.  
 CC CHAIN 1 234  
 CC FT CHAIN 8 234  
 CC FT INIT\_MET 8 234  
 CC FT DOMAIN 48 218  
 CC FT TRANSMEM 1 53  
 CC FT DOMAIN 54 74  
 CC FT TRANSMEM 75 97  
 CC FT TRANSMEM 98 118  
 CC FT DOMAIN 119 122  
 CC FT TRANSMEM 123 143  
 CC FT DOMAIN 144 150  
 CC FT TRANSMEM 151 171  
 CC FT DOMAIN 172 234  
 CC SQ SEQUENCE 234 AA; 26654 MW; AFB7DAE31983FB0 CRC64;

Query Match 100.0%; Score 1195; DB 1; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-100;  
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNHLPEBMENALTSQSSHSALRWHSINPOLMARIESYGRKKGISDVRFFCFEVT 60  
 DB 1 MNHLPEBMENALTSQSSHSALRWHSINPOLMARIESYGRKKGISDVRFFCFEVT 60  
 QY 61 FDLLEFVTLVLIILNVNGGIEENTLEKEVMQYDYSSYFDIFLLAVFRPKVLLAVAVCRL 120  
 DB 61 FDLLEFVTLVLIILNVNGGIEENTLEKEVMQYDYSSYFDIFLLAVFRPKVLLAVAVCRL 120  
 QY 121 RHWWAIALTRAVTSAPFLAKVILSKLFSQCAFGLVPLIISFIILAMISTWFDLFLVLPQEA 180  
 DB 121 RHWWAIALTRAVTSAPFLAKVILSKLFSQCAFGLVPLIISFIILAMISTWFDLFLVLPQEA 180  
 QY 181 EENRRLIIVDASRRALIPGGLSDGQFYSPPSEASESEKKEKDEKPLEL 234  
 DB 181 EENRRLIIVDASRRALIPGGLSDGQFYSPPSEASESEKKEKDEKPLEL 234

RESULT 2  
 ID MENT\_MOUSE STANDARD; PRT; 235 AA.  
 AC Q9DCI3; Q9J463; Q9J356;

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE MN64 N-terminal domain homolog (STARD3 N-terminal like protein).  
 GN Name=stard3; Synonyms=Mentho;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum; and Kidney;  
 RX MEDLINE=22354683; Pubmed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki I., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Betzel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chochla C., Corbett L.E., Cousins S.,  
 RA Dalia E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Guellincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Meglert D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yamagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kikukawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino Y.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=22368257; Pubmed=12477932; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toibiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huijck S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J.J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal  
 CC membrane protein (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9DCI3-1; Sequence=Displayed;  
 CC Name=2;



RA SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
RA Strauberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Mannina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stepieton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiluyki S., Carninci P., Prange C.,  
RA Rana S.S., Lequellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywnicki M.I., Skaleka U., Smallus D.E., Schermer A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Strauberg R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC075752; AAH5752.1; -  
SQ SEQUENCE 227 AA; 25485 MW; 24C46ADBFF4985C6 CRC64;  
  
Query Match 66.6%; Score 796; DB 2; Length 227;  
Best Local Similarity 68.3%; Pred. No. 5.1e-64;  
Matches 155; Conservative 31; Mismatches 39; Indels 2; Gaps 2  
  
QY 8 MENALTGSQSSHAGLRINIHNSINPTQWLARISSYSGREKKGISDVRRTECLFTVPTDLFTY 67  
Db 1 MDSCSSSVSGSRALVGGIGGNINSTPISRAVSEYRAGEKKGISDVRRTECLFTVPTDLFTY 60  
QY 68 LMTWIELNVNGGIENTLEKEVMQDYDYSYEDIFLLAVFRFKVILLAYAVCRLRHMAA 127  
Db 61 LMTWIELNVNGGIGQQLQEQLEVLTKTDYHKSFPDIFLLAVFRALILLAYAVCKLRHMAA 120  
QY 128 LTTAVTSATFLAKYISKLSQSGAFGVLPITISLTANIEFWLPDFKLPQBAEENRLL 187  
Db 121 ITTATITGFGPIVKKVVSFKLSQSGAFGVLPITISLTANIEFWLPDFKLPQBAEGEIRYL 180  
QY 188 IYVDASRALI-PCGSLDQGFVSPPESEGS-EEAEKQSEKRPRL 232  
Db 181 SVGNRLHEHPLPPGPLESGLFYSPPESLADSDLDLDDKPLDEKPIV 227  
  
RESULT 4  
O6DFR7 PRELIMINARY; PRT; 448 AA.  
AC O6DFR7;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Starch-prov protein.  
GN Name=starch-prov;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodidae; Xenopus.  
OX NCBI\_TaxID=8364;  
RX [1] -  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX PubMed=12477932; DOI=10.1073/pnae.242603899;  
RA Strauberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisano K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Kzywnski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC076666; AAH76666.1; -  
 DR GO; GO:0015485; F:cholesterol binding; IEA.  
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.  
 DR GO; GO:0006694; P:steroid biosynthesis; IEA.  
 DR InterPro; IPR007999; SCAR.  
 DR InterPro; IPR002913; START.  
 DR PRINTS; PRO0978; STARPROTEIN.  
 DR SMART; SM00234; START; 1.  
 DR PROSITE; PS50848; START; 1.  
 SQ SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;  
 Query March 58.6%; Score 700.5; DB 2; Length 448;  
 Best Local Similarity 61.1%; Pred. No. 5.2e-55;  
 Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;  
 QY 1 MNHLP---EDMENALTGSSSHASLNNHSINPTQLMARIESYEGREKKGISDVRRTPC 56  
 DB 1 MTKLPGFQFDLERSLPALASINSMSQNHVFSHSLPR-----EQRVIVSVRRTPC 54  
 QY 57 LFVTFDLFTLMTILANNNGIENLEKEMQYDYSSYFDIPLAVRPFKVLIIAYA 116  
 DB 55 LFVTFDLFTLMTILANNNGIENLEKEMQYDYSSYFDIPLAVRPFKVLIIAYA 114  
 QY 117 VCRRLHMAIALTTAVTSAPFLAKVILSKLPSQAGFVPIISFIILAMETWFLDPKVL 176  
 DB 115 IVRLRHMAIALTTAVTSAPFLAKVILSKLPSQAGFVPIISFIILAMETWFLDPKVL 174  
 QY 177 PQEAEEENRLLIYQDASERAAI-L-PGGLSDQGFYSPESSEAGSEAEKODSEK 229  
 DB 175 TQEAEEERWMAVQAGSHPLLYNGALSDQGFYSPESSEAGSD--NEPDDEE 226  
 RESULT 5  
 Q6PFA0 PRELIMINARY; PRT; 444 AA.  
 AC O6PFA0;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DE MGC68989 protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MDLINE=3238625; PubMed=12477937; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisano K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Kzywnski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MDLINE=32341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Klein S., Strausberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC057738; AAH57738.1; -  
 DR GO; GO:0015485; F:cholesterol binding; IEA.  
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.  
 DR GO; GO:0006694; P:steroid biosynthesis; IEA.  
 DR InterPro; IPR007999; SCAR.  
 DR InterPro; IPR002913; START.  
 DR PRINTS; PRO0978; STARPROTEIN.  
 DR SMART; SM00234; START; 1.  
 DR PROSITE; PS50848; START; 1.  
 SQ SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;  
 Query March 58.5%; Score 698.5; DB 2; Length 444;  
 Best Local Similarity 60.9%; Pred. No. 7.9e-55;  
 Matches 140; Conservative 30; Mismatches 51; Indels 9; Gaps 3;  
 QY 1 MNHLPEDMENALTGSSSHASLNNHSINPTQLMARIESYEGREKKGISDVRRTPC 60  
 DB 1 MTKLPGFQFDLERSLPALASINSQSHVFSRSLPR-----EQRVIVSVRRTPC 54  
 QY 61 FDLFTLMTILANNNGIENLEKEMQYDYSSYFDIPLAVRPFKVLIIAYVCR 120  
 DB 55 FDLFTLMTILANNNGIENLEKEMQYDYSSYFDIPLAVRPFKVLIIAYVCR 114  
 QY 121 RHWMAIALTTAVTSAPFLAKVILSKLPSQAGFVPIISFIILAMETWFLDPKVL 180  
 DB 115 RHWMAIALTTAVTSAPFLAKVILSKLPSQAGFVPIISFIILAMETWFLDPKVL 174  
 QY 181 EENRRLLIYQDASERAAI-L-PGGLSDQGFYSPESSEAGSEAEKODSEK 229  
 DB 175 EEBRWYIAQAAATPHSLLYNGALSDQGFYSPESSEAGSD--NEPDDEE 222  
 RESULT 6  
 Q6GNT3 PRELIMINARY; PRT; 448 AA.  
 ID Q6GNT3;  
 AC O6GNT3;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DE MGC68985 protein.  
 GN Name=MGC68985;





RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Binds and transports cholesterol. Promotes  
 CC steroidogenesis in placenta and brain (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal  
 CC membrane protein (By similarity).  
 CC -1- SIMILARITY: Contains 1 MEMBRAN domain.  
 CC -1- SIMILARITY: Contains 1 START domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

DR EMBL: X82457; CA57834.1; -.  
 DR EMBL: BC003313; AAH03313.1; -.  
 DR HSSP: Q14848; 1EM2.  
 DR MGD; MG1:1929618; Stard3.  
 DR InterPro; IPR000799; STAR.  
 DR InterPro; IPR002913; STAR.  
 DR Pfam; PF01852; START; 1.  
 DR PRINTS; PR00978; STARPPOTEIN.  
 DR SMART; SM00234; START; 1.  
 DR PROSITE; PS50848; START; 1.  
 DR KX Lipid transport; lipid-binding; Steroidogenesis; Transmembrane;  
 DR KX Transport.  
 FT DOMAIN 1 52 Cytoplasmic (Potential).  
 FT TRANSMEM 53 73 Potential.  
 FT DOMAIN 74 95 Extracellular (Potential).  
 FT TRANSMEM 96 116 Potential.  
 FT DOMAIN 117 121 Cytoplasmic (Potential).  
 FT TRANSMEM 122 142 Potential.  
 FT DOMAIN 143 149 Extracellular (Potential).  
 FT TRANSMEM 150 170 Potential.  
 FT DOMAIN 171 446 Cytoplasmic (Potential).  
 FT DOMAIN 47 218 Potential.  
 FT DOMAIN 231 444 START.  
 SQ SEQUENCE 446 AA; 50469 MW; DBF4359604F3E1E2 CRC64;

Query Match 54.9%; Score 656.5; DB 1; Length 446;  
 Best Local Similarity 57.8%; Pred. No. 5.1e-51;  
 Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;

QY 7 DMENAL-----TSSQSSHASLRNHSINPTQLMARIESYEGREKSGIDVRRTECLFVT 61  
 Db 11 DLERSLPALASLSTSHSGLSHSRTPPL-----EKRRASDVRRTECLFVT 60  
 QY 62 DLLFTVLLMIIEINVGIIENLEKEVMQDYSSYDFLLAVFRPKVILIAVACRLR 121  
 Db 61 DLLFISLMIIEINVTGIRKNEQEVYHSFQSPFDIVLAFFRPSGLLGAVALRLQ 120  
 QY 122 HMAAALTTVAATFLLAKVILSKLPSQAGVYLPIISFTLMIEMWFLDFVLPQEAR 161  
 Db 121 HMAVIAATTVSSAFLVAVILSKLPSQAGVYLPIISFTLMIEMWFLDFVLPQEAR 160  
 QY 182 EENRLIVDASERAAI-PSGLSDGQFYSPSEASGE-EAEKQDSEK 229  
 Db 181 EENWYLAQAQAVARGPLLPSGLSSEGFYSPSEASGEDEVTGKK 230

RESULT 9  
 Q6PH03 PRELIMINARY; PRT; 448 AA.

AC Q6PH03; (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE START domain containing 3.  
 GN Name=stard3;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OK NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=whole body;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maria M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=whole body;  
 RA Strausberg R.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC056766; AAH56766.1; -.  
 DR ZFIN; ZDB-GENE-001120-2; stard3.  
 DR GO; GO:0015485; F:cholesterol binding; IEA.  
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.  
 DR GO; GO:0006944; P:steroid biosynthesis; IEA.  
 DR InterPro; IPR000799; STAR.  
 DR InterPro; IPR002913; STAR.  
 DR Pfam; PF01852; START; 1.  
 DR PRINTS; PR00978; STARPPOTEIN.  
 DR SMART; SM00234; START; 1.  
 DR PROSITE; PS50848; START; 1.  
 DR SEQUENCE 448 AA; 50751 MW; 716A18C127B59C5D CRC64;

Query Match 52.9%; Score 632; DB 2; Length 448;  
 Best Local Similarity 70.9%; Pred. No. 8.6e-49;  
 Matches 127; Conservative 18; Mismatches 32; Indels 2; Gaps 2;

QY 44 EKKGIDVRRTECLFVTFDILLFTLLMIIEINVGIIENLEKEVMQDYSSYDFILL 103  
 Db 43 ERKAFSDVRRTECLFVTFDILLFTLLMIIEINLSKSIWNSLENEVHYNKSFFDFILL 102  
 QY 104 AVRFKVLIAAVVCGLRHMAATLTAATVSAFLAKVILSKLPSQAGVYLPIISFIL 163  
 Db 103 AVRFKVLIAAVVCGLRHMAATLTAATVSAFLAKVILSKLPSQAGVYLPIISFV 162  
 QY 164 AMIETVFLDFKVLVQAEEN-RLILVODASERAAI-PSGLSDGQFYSPSEASGE 220  
 Db 163 AMIETVFLDFKVLVQAEEN-RLILVODASERAAI-PSGLSDGQFYSPSEASGE 221

RESULT 10  
 Q6BMP8 PRELIMINARY; PRT; 107 AA.

AC OGBMP8;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length  
 DE enriched library, clone:530402M06 product:H.NH021A08.1 PROTEIN  
 DE (UNKNOWN) (PROTEIN FOR MGC:14607) (SIMILAR TO STEROIDGENIC ACUTE  
 DE REGULATORY PROTEIN RELATED) homolog.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carminci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Mech. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;  
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carminci P., Shihata Y., Hayatsu N., Sugahara Y., Shihata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shihata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carminci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitasuna T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujisawa S., Inoue K., Togawa Y., Iwawa M., Ohara E., Matsuki M.,  
 RA Yoneda Y., Ishiura T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=pituitary gland;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carminci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiseoka T., Hirozane T.,  
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnaka N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shihata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tasaka A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK030365; BAC26922.1; -.

SQ SEQUENCE 107 AA; 12417 MW; 1B30DA6C81469089 CRC64;  
 Query Match 41.2%; Score 492; DB 2; Length 107;  
 Best Local Similarity 92.2%; Pred. No. 8.2e-37;  
 Matches 94; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MNHLPEDMENALTGSSGSHASLRNHSINPTQLMARIESYEGREKGISVRRTPCLFVT 60  
 DB 1 MNHLPEDMENALTGSSGSHASLRNHSINPTQLMARIESYEGREKGISVRRTPCLFVT 60  
 QY 61 FDLFPVTLMTIELNVNGGIENTLEKEVMQYDYSSYFDLFL 102  
 DB 61 FDLFPVTLMTIELNVNGGIENTLEKEVMQYDYSSYFDLFL 102

RESULT 11  
 Q7QIT3 PRELIMINARY; PRT; 568 AA.  
 AC Q7QIT3;  
 DT 01-MAR-2004 (TReMBLrel. 26, Created)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
 DE AgCP3158 (Fragment).  
 GN Name=agc32468; ORFNames=ENSG00000018959;  
 OS Anopheles gambiae str. FST.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
 ON NCBI\_TaxID=180454;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PEST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAB01008807; EAA03945.1; -  
 DR GO; GO:0015485; F:cholesterol binding; IEA.  
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.  
 DR GO; GO:0006694; P:steroid biosynthesis; IEA.  
 DR InterPro: IPR000799; STAR.  
 DR InterPro: IPR002913; STAR.  
 DR PRINTS; PRO0976; STARRPROTEIN.  
 DR PROSITE; PSS0848; START; 1.  
 FT NON TER 1  
 FT NON TER 568  
 SQ SEQUENCE 568 AA; 62932 MW; ECB3D361A05DF15 CRC64;  
 Query Match 29.1%; Score 348; DB 2; Length 568;  
 Best Local Similarity 36.6%; Pred. No. 6.7e-23;  
 Matches 86; Conservative 45; Mismatches 72; Indels 32; Gaps 9;  
 QY 13 TGSOSHASLRNHSINPTQLMAR--IESYEGREKGISVRRTPCLFVTDLFLVTLW 70  
 DB 1 TRSQS-----HYNA--LISEDFLAG--MEGRMSVRRFCLFVTFDVFLSLW 47  
 QY 71 IIEIANVNG-GIENTLEKEVMQYDYSSYFDLFLAVFRFKVLILAYAVCRHWMALAT 129  
 DB 48 IICVITGDVNHALQTVLHYTVYTSLFDVIALIRFLILFGLISISHMLVALS 107  
 QY 130 TAVTSAPLAKVLISLKLFS--QCAFQVLPILIFILAMFTWLDKVLPOQEAEENRLL 167  
 DB 108 TTSCSCLFLSKVLPYDWTATPQVFVLLIVSFVLAWGAWFLDKCRVLPQERFARVYFV 167  
 QY 188 IYVDASERALLP-----GGLSD--GCFYSPES--EAGSEBAEKQDSE 228  
 DB 168 AITNPGSMARKTFLPLPFLSAMQAGRTESIGNYSPFDSIHNSDDDDDDDDDDQDDE 222

RESULT 12  
 Q8MZ4 PRELIMINARY; PRT; 545 AA.  
 AC Q8MZ4;







OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.P.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,  
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Botkina D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,  
 RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,  
 RA Hartz N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,  
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,  
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zeng X.H., Zheng F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frishe E., Hodgson A.,  
 RA George R.A., Hoekins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 RT *melanogaster* euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Celniker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frishe E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu U., Berman B.P.,  
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX FLYBASE;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX FLYBASE;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14745013; DOI=10.1073/pnas.0308212100;  
 RA Roth G.E., Gierl M.S., Vollborn L., Meise M., Lintermann R., Korge G.,  
 RT "The *Drosophila* gene *Starl*: a putative cholesterol transporter and  
 RT key regulator of ecdysteroid synthesis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:1601-1606(2004).  
 DR EMBL: AE003464; AAF47232.2; -;  
 DR EMBL: AY455866; AAR19767.1; -;  
 DR InAct: Q9W145; -;  
 DR FLYBASE: FBgn0035028; CG3522.  
 DR GO: GO:0015485; F:cholesterol binding; IEA.  
 DR GO: GO:0017127; F:cholesterol transporter activity; IEA.  
 DR GO: GO:0006694; P:steroid biosynthesis; IEA.  
 DR InterPro: IPR000799; STAR.  
 DR InterPro: IPR002913; START.  
 DR Pfam: PF01852; START.  
 DR PRINTS: PR00978; STARPOTEIN.  
 DR PROSITE: PSS0848; START; 1.  
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 Best Local Similarity 37.8%; Pred. No. 2e-22;  
 Matches 90; Conservative 44; Mismatches 76; Indels 28; Gaps 10;  
 QY 8 MENALQSOSGSA--SLRNHSINPTOLMARISYSGREKKG-ISPDRFTCLFTVFDLL 64  
 DB 17 LANARQGNAYNQYDMRSRASHN---LTFEFLAGYMGDGMSTVVRFFCLFTVFDLV 72  
 QY 65 FVTLLWITIELVNG--GIENLTKENVQYDYSYFDFILLAVRFFVLLIAYVCELRHW 123  
 DB 73 FVSLWMLICIVNGDNIFFAFHKOIYEITYKSLFVAVAVACRFLIFPFAIIVYNHW 132  
 QY 124 WALALTATVATSLAKVIL-----SKLPSQAGFVGLPIISITLMIETWTFDFVLPO 178  
 DB 133 SIATLSTSGSCLPLISKVFFVFWLDSK---QVFEVILLITSTFLMGEAMFLDCRVLPQ 189  
 QY 179 B--AEENRRLIYQDAS--ERALLI-----PGSLDQGFSPSEBAGSEAEKRD 226  
 DB 190 ERRAQHYFRMTSNDRTPEQPAILLERPPQSVTD--FSLMDTARRHSDDEDDDD 245  
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 019819  
 ID 019819 PRELIMINARY; PRT; 447 AA.  
 AC 019819  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-OCT-2002 (TEMBLrel. 22, last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)  
 DE Hypothetical protein F26F4.4.  
 OS ORFNames=F26F4.4, F26F4.4;  
 GN Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Br16C01 N2;  
 MEDLINE=99069613; PubMed=9851916;

RG WormBase Consortium;  
 RT "Genome sequence of the nematode *C. elegans*: a platform for  
 RT investigating biology. The *C. elegans* Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Pullon L.;  
 RT "The sequence of *C. elegans* cosmid F26F4.";  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wilson R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RG WormBase Consortium;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U12964; AAA91219.3; -.  
 DR PIR; T16170; T16170.  
 DR WormBase; WGene00017626; F26F4.4.  
 DR WormPep; F26F4.4; CE30767.  
 DR InterPro; IPR002913; START.  
 DR Pfam; PF01852; START; 1.  
 DR SMART; SM00234; START; 1.  
 DR PROSITE; PSS0848; START; 1.  
 DR Hypothetical protein.  
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 Best Local Similarity 26.5%; Pred. No. 5.9e-10;  
 Matches 56; Conservative 36; Mismatches 73; Indels 46; Gaps 6;  
 QY 42 GREKGISDVRRPCLFVTPDLLFVTLMLTI-----ELNVNGIENLEK 86  
 DB 11 GSQRIGVSKDKRPFIVTFDTISITLLMLCTVTRDDWDKVPFNEINI-----FNP 63  
 QY 87 EVMQYDYSSYPDIFPLAVRFRKYLILAYVCRLRHWMALATTAVTSAFLAKVILSK 146  
 DB 64 KPIRI-----SLFDIVLLAVLRMLILGVYGCIVKQWYVAFTTLASSAYILMKVLPYFN 119  
 QY 147 PSQCAFQGVLPPI-SFILAWIETWFLDFKYLPOEAEENRLLIVQDASERAILPGGLSD 205  
 DB 120 HSSSAVPEPLLIITTSFTLCSSEFLMPFQILPRRRYARREL-----DGIEN 166  
 QY 206 GQFYSPPESEA-----GSEEAEEKDSEKP 230  
 DB 167 PEPSTDDARSNNRRRGRQNGNSQSEAP 197  
 RESULT 15  
 ML64\_SALFO STANDARD; PRT; 294 AA.  
 AC O902B9;  
 DT 28-FEB-2003 (Rel. 41, Last Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE MLN64-like protein (Fragment).  
 GN Name=MLN64;  
 OS Salvelinus fontinalis (Brook trout) (Brook char).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.  
 OC NCBI\_TaxID=8038;  
 OX 1)  
 RN SEQUENCE FROM N.A.

RA Goetz F.W.;  
 RT "Cloning and characterization of trout MLN64.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Binds and transports cholesterol. Promotes  
 CC steroidogenesis (by similarity).  
 CC -1- SIMILARITY: Contains 1 START domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; AF264379; AA82981.1; -.  
 DR InterPro; IPR000799; STAR.  
 DR InterPro; IPR002913; START.  
 DR Pfam; PF01852; START; 1.  
 DR PRINTS; PR00976; STARPROTEIN.  
 DR SMART; SM00234; START; 1.  
 DR PROSITE; PSS0848; START; 1.  
 DR Lipid transport; Lipid-binding; Steroidogenesis; Transport.  
 KW NON TER 1  
 FT DOMAIN 1 292 START.  
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 Best Local Similarity 66.7%; Pred. No. 0.39;  
 Matches 24; Conservative 3; Mismatches 8; Indels 1; Gaps 1;  
 QY 186 LLIVQDASERAIL-PGLSDGQFYSPPESEAGSEE 220  
 DB 33 LAAVNAASERAPMITYRAVSEGGFYSPPESLAGSEE 68

Search completed: May 17, 2005, 10:24:41  
 Job time : 106 secs

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# OM protein - protein search, using sw model

Run on: May 17, 2005, 10:15:40 ; Search time 17 seconds  
(without alignments)  
1324.395 Million cell updates/sec

Title: US-10-063-518-14  
Perfect score: 1195  
Sequence: 1 MNHLPPDMNALTGSSQSHA.....EAGSEAEKQDEKPLEL 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	664	55.6	445	2	138027
2	204	17.1	478	2	116170
3	102.5	8.6	348	2	H90281
4	93.5	7.8	424	2	D75080
5	90	7.5	1911	2	T43048
6	86.5	7.2	767	2	T21969
7	85.5	7.2	366	2	B81299
8	85.5	7.2	438	2	A57219
9	85	7.1	448	2	G70172
10	84.5	7.1	471	2	A41680
11	83.5	7.0	352	2	H97002
12	83	6.9	291	2	AE0302
13	83	6.9	590	1	S34960
14	82.5	6.9	186	1	B29835
15	82.5	6.9	239	1	C64227
16	82.5	6.9	341	2	S51265
17	82.5	6.9	406	2	T43130
18	82.5	6.9	891	2	T37397
19	82	6.9	589	2	T52070
20	82	6.9	589	2	A36963
21	82	6.9	1466	2	T30566
22	81	6.8	385	2	B84447
23	81	6.8	529	2	T23130
24	81	6.8	532	2	S46831
25	80.5	6.7	156	2	T84498
26	80.5	6.7	322	2	T45568
27	80.5	6.7	322	2	T50229
28	80.5	6.7	417	2	C44038
29	80.5	6.7	463	2	AE1155

30	80.5	6.7	536	2	A71491	probable integral
31	80.5	6.7	644	2	S63056	probable membrane
32	80.5	6.7	738	2	S10659	membrane protein t
33	80.5	6.7	891	1	MNV235	major core protein
34	80.5	6.7	891	1	MNV235	major core protein
35	80.5	6.7	1780	2	A85045	probable glycan sy
36	80	6.7	103	2	G75513	conserved hypotnet
37	80	6.7	290	2	D89898	hypothetical prote
38	80	6.7	309	2	S59140	RTM1 protein - Yea
39	80	6.7	388	2	H71115	hypothetical prote
40	80	6.7	1339	2	A84683	probable SNF2 bndf
41	79.5	6.7	463	2	AH1513	amino acid transpo
42	79.5	6.7	491	1	EDBERC	immediate-early pr
43	78.5	6.6	239	2	S73812	hypothetical prote
44	78.5	6.6	269	2	AF1532	spermidine/putresc
45	78.5	6.6	358	2	F64136	rtfd protein homol
46	78.5	6.6	471	2	S11280	serotonin receptor
47	78.5	6.6	678	2	S44925	IB3/5-polyepitide
48	78	6.5	245	2	JC5346	cdd2 protein - Clo
49	78	6.5	259	2	F83825	hypothetical prote
50	78	6.5	382	2	E97157	stage III sporulat
51	78	6.5	471	2	B64089	undecaprenyl-phosp
52	78	6.5	1297	2	T39287	hypothetical prote
53	78	6.5	2136	2	A05037	hypothetical prote
54	77.5	6.5	269	2	AH1175	spermidine/putresc
55	77.5	6.5	299	2	AE0461	probable membrane
56	77.5	6.5	327	2	F82904	conserved hypotnet
57	77.5	6.5	328	2	F84130	ABC transporter (p
58	77.5	6.5	338	2	T39159	hypothetical prote
59	77.5	6.5	440	2	T11319	NMDH2 dehydrogenas
60	77.5	6.5	491	2	B69499	sodium- and chlori
61	77.5	6.5	512	2	AC3399	probable colanic b
62	77.5	6.5	734	1	DERZM5	NMDH2 dehydrogenas
63	77.5	6.5	892	2	H72164	ALL protein - var
64	77.5	6.5	892	2	T28552	hypothetical prote
65	77.5	6.5	892	2	B36849	hypothetical prote
66	77.5	6.5	1784	2	T43167	A10L protein - var
67	77	6.4	332	2	T23307	sodium channel pro
68	77	6.4	559	2	C87307	hypothetical prote
69	77	6.4	590	1	QOUTC5	hypothetical prote
70	77	6.4	650	2	A90072	NMDH2 dehydrogenas
71	77	6.4	991	2	T01377	hypothetical prote
72	77	6.4	1025	2	T18376	multidrug resistan
73	77	6.4	1117	2	C85018	hypothetical prote
74	77	6.4	1500	2	G84922	hypothetical prote
75	76.5	6.4	278	2	B85807	probable tail fibre
76	76.5	6.4	278	2	H90958	probable tail fibre
77	76.5	6.4	282	2	H95869	probable sugar ABC
78	76.5	6.4	352	2	T25170	hypothetical prote
79	76.5	6.4	352	2	AF0692	probable membrane
80	76.5	6.4	494	2	JC5919	potassium channel
81	76.5	6.4	538	2	B81435	probable iron-upca
82	76.5	6.4	589	2	A71918	probable secretion
83	76.5	6.4	646	2	T41545	hypothetical trans
84	76	6.4	342	2	T11476	NMDH2 dehydrogenas
85	76	6.4	402	2	T24184	hypothetical prote
86	76	6.4	669	2	T48466	hypothetical prote
87	76	6.4	1402	2	T24664	hypothetical prote
88	76	6.4	1450	2	JC6139	cyclic fibrosis tr
89	76	6.4	1783	2	T37258	probable voltage cl
90	76	6.4	1917	2	C88728	protein C48A7.1 (l
91	75.5	6.3	156	2	T62107	melatonin receptor
92	75.5	6.3	263	2	G95198	hypothetical prote
93	75.5	6.3	263	2	C98085	hypothetical prote
94	75.5	6.3	339	2	B82211	conserved hypotnet
95	75.5	6.3	352	2	H64919	probable membrane
96	75.5	6.3	352	2	G85769	hypothetical prote
97	75.5	6.3	352	2	C90921	hypothetical prote
98	75.5	6.3	415	2	F91209	low affinity trypt
99	75.5	6.3	415	2	A86056	low affinity trypt
100	75.5	6.3	415	2	A39412	tryptophan transp
101	75.5	6.3	471	2	S40689	5-hydroxytryptamin
102	75.5	6.3	498	2	T11039	NMDH2 dehydrogenas

103	75.5	6.3	593	2	H64594	multidrug resistan
104	75.5	6.3	708	2	T29669	hypothetical prote
105	75.5	6.3	775	2	T52107	anion channel prot
106	75.5	6.3	1142	2	T93103	probable negative
107	75	6.3	249	2	G64470	sulfate/chitosulfat
108	75	6.3	274	2	A82509	probable phosphat
109	75	6.3	330	2	B71163	probable oligopept
110	75	6.3	473	2	A38627	gamma-aminobutyric
111	75	6.3	526	2	T45850	hypothetical prote
112	75	6.3	649	2	G69810	anion-binding prot
113	75	6.3	753	2	H90124	hypothetical prote
114	75	6.3	2248	1	D42088	adenylate cyclase
115	74.5	6.2	276	2	A95881	probable trehalose
116	74.5	6.2	335	2	H73420	oligopeptide ABC c
117	74.5	6.2	355	2	JC4304	orphan G protein-c
118	74.5	6.2	471	2	A34863	serotonin receptor
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter
120	74.5	6.2	500	2	T14826	transcription init
121	74.5	6.2	574	2	T05964	probable low-affin
122	74.5	6.2	618	1	S38004	probable transport
123	74.5	6.2	1808	2	T47792	hypothetical prote
124	74	6.2	231	1	G69540	cobalamin (5'-phos
125	74	6.2	231	1	B69422	quinone-reactive N
126	74	6.2	281	1	S26018	NMDH2 dehydrogenas
127	74	6.2	286	1	S73424	spermidine/putresc
128	74	6.2	312	2	C72547	probable aspartate
129	74	6.2	312	2	H86732	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto
131	74	6.2	350	2	T38848	Mel-1a melanotin r
132	74	6.2	356	2	H89869	hypothetical prote
133	74	6.2	442	2	C86859	transmembrane effi
134	74	6.2	449	2	S02011	serotonin receptor
135	74	6.2	475	2	T36137	probable amino aci
136	74	6.2	485	2	T24115	hypothetical prote
137	74	6.2	487	1	C71417	cytochrome P450 d1
138	74	6.2	493	2	JC7378	L-lysine 6-aminotr
139	74	6.2	1123	2	T51517	telomerase reverse
140	73.5	6.2	153	2	E95845	conserved hypochet
141	73.5	6.2	192	2	A84727	hypothetical prote
142	73.5	6.2	216	2	G70474	hypothetical prote
143	73.5	6.2	318	2	S76713	hypothetical prote
144	73.5	6.2	338	2	T40448	conserved hypochet
145	73.5	6.2	379	2	S58448	ubiquitinol-cytochro
146	73.5	6.2	384	2	AF0636	glucanase biosynthes
147	73.5	6.2	385	1	S01511	ubiquitinol-cytochro
148	73.5	6.2	385	1	A69804	ABC transporter (A
149	73.5	6.2	413	2	AD1738	similar to multidr
150	73.5	6.2	442	2	C96672	hypothetical prote
151	73.5	6.2	491	1	EDBEK5	immediate-early pr
152	73.5	6.2	634	2	F82623	potassium uptake p
153	73.5	6.2	637	2	H83945	DNA mismatch repai
154	73.5	6.2	640	2	B32935	hypothetical prote
155	73.5	6.2	731	2	T31914	hypothetical prote
156	73.5	6.2	1095	2	E96744	probable oligopept
157	73.5	6.2	1174	2	A39927	RNA-directed RNA p
158	73	6.1	114	2	F71925	cag island protein
159	73	6.1	282	2	S26030	NMDH2 dehydrogenas
160	73	6.1	339	2	T15560	hypothetical prote
161	73	6.1	450	1	M2B8E4	49.2K membrane pro
162	73	6.1	453	2	T30985	hypothetical prote
163	73	6.1	553	2	A71823	hypothetical prote
164	73	6.1	788	2	G89901	hypothetical prote
165	73	6.1	971	2	T00268	hypothetical prote
166	73	6.1	1075	2	B96508	hypothetical prote
167	73	6.1	6805	2	S20901	titin - rabbit (fr
168	72.5	6.1	209	2	S72929	hypothetical prote
169	72.5	6.1	222	2	B85866	probable transport
170	72.5	6.1	222	2	B91022	probable transport
171	72.5	6.1	222	2	H64996	ubiquitinol-cytochro
172	72.5	6.1	255	2	A60944	ubiquitinol-cytochro
173	72.5	6.1	291	2	T02986	chlorophyll a/b-bi
174	72.5	6.1	307	2	A86596	conserved hypochet
175	72.5	6.1	315	2	H96598	protein F20M2.8 [1
176	72.5	6.1	325	2	H86670	hypothetical prote
177	72.5	6.1	336	2	C88951	protein C38C3.2 [1
178	72.5	6.1	389	2	A55493	oxytocin receptor
179	72.5	6.1	428	2	AF0173	probable paracuat-
180	72.5	6.1	499	2	H70453	virulence factor M
181	72.5	6.1	513	2	S47631	pituitary adenylat
182	72.5	6.1	522	2	T29705	hypothetical prote
183	72.5	6.1	635	2	T23465	hypothetical prote
184	72.5	6.1	718	2	S57913	probable transloca
185	72.5	6.1	749	2	C84508	probable cap-bindi
186	72.5	6.1	749	2	T30037	hypothetical prote
187	72.5	6.1	1539	2	T21099	hypothetical prote
188	72	6.0	279	2	AB1156	hypothetical prote
189	72	6.0	306	2	AB1156	hypothetical prote
190	72	6.0	339	2	G97199	probable peptidase
191	72	6.0	377	2	T27805	hypothetical prote
192	72	6.0	379	2	T27805	ubiquitinol-cytochro
193	72	6.0	415	1	MMAD52	late L1 52K protei
194	72	6.0	433	2	T39155	glycosyl hydrolase
195	72	6.0	453	2	D89760	conserved hypochet
196	72	6.0	479	2	S64587	hypothetical prote
197	72	6.0	497	2	G96611	probable cytochrom
198	72	6.0	514	2	T15338	hypothetical prote
199	72	6.0	534	2	T42660	hypothetical prote
200	72	6.0	600	2	T39673	hypothetical prote
201	72	6.0	630	2	T07966	probable ethylene
202	72	6.0	1038	2	S37854	hypothetical prote
203	72	6.0	1094	2	S22573	DNA-directed DNA p
204	72	6.0	1113	2	T20140	hypothetical prote
205	72	6.0	1220	2	T18291	patched protein -
206	72	6.0	1275	2	UU0092	crp protein - fru1
207	72	6.0	1282	2	T30804	P-glycoprotein 6 -
208	71.5	6.0	210	2	S52050	cytochrome-c oxida
209	71.5	6.0	225	1	MMH68	beta membrane glycop
210	71.5	6.0	237	2	H70975	hypothetical prote
211	71.5	6.0	246	2	AG3544	flagellar biosynth
212	71.5	6.0	301	2	F86647	hypothetical prote
213	71.5	6.0	341	2	F90084	hypothetical prote
214	71.5	6.0	345	2	T33706	hypothetical prote
215	71.5	6.0	348	2	D82252	RnfD-related prote
216	71.5	6.0	355	2	AB3516	sensory transducti
217	71.5	6.0	352	2	S48689	prostaglandin E(2)
218	71.5	6.0	366	2	S51280	EP3-alpha receptor
219	71.5	6.0	366	2	I46469	Mel-1a melanotin r
220	71.5	6.0	381	2	T11776	ubiquitinol-cytochro
221	71.5	6.0	383	2	T38194	hypothetical prote
222	71.5	6.0	386	1	S34043	oxytocin receptor
223	71.5	6.0	390	2	S66497	isotocin receptor
224	71.5	6.0	435	2	AD1340	maltoedextrin ABC-c
225	71.5	6.0	435	2	AB1711	maltoedextrin ABC-c
226	71.5	6.0	471	2	PS0154	125K surface antig
227	71.5	6.0	510	2	T10124	hexose transport p
228	71.5	6.0	524	2	T02499	hypothetical prote
229	71.5	6.0	603	2	H90061	hypothetical prote
230	71.5	6.0	651	2	T46050	hypothetical prote
231	71.5	6.0	659	2	D64137	bet1 protein homol
232	71.5	6.0	670	2	A49580	meditaeas transport
233	71.5	6.0	823	2	T34472	hypothetical prote
234	71.5	6.0	1407	2	B42239	adenylate cyclase
235	71.5	6.0	3010	1	S18030	genome polyprotein
236	71	5.9	114	2	H64586	cag pathogenicity
237	71	5.9	225	1	MMHAI1	beta membrane glycop
238	71	5.9	250	2	A82367	conserved hypochet
239	71	5.9	258	2	AB1355	probable processin
240	71	5.9	290	2	S33443	chlorophyll a/b-bi
241	71	5.9	339	2	T16745	hypothetical prote
242	71	5.9	345	2	T12372	NMDH2 dehydrogenas
243	71	5.9	345	2	T25561	hypothetical prote
244	71	5.9	361	2	C90603	hypothetical prote
245	71	5.9	391	2	F86759	hypothetical prote
246	71	5.9	416	2	E87286	3-deoxy-D-manno-oc
247	71	5.9	423	2	AF1335	transcription regu
248	71	5.9	471	2	A43956	serotonin receptor

249	71	5.9	546	2	S48932	hypothetical prote
250	71	5.9	563	2	T38766	probable transcrip
251	71	5.9	576	2	T32509	hypothetical prote
252	71	5.9	620	2	A58932	cytochrome C-type
253	71	5.9	676	2	E96725	hypothetical prote
254	71	5.9	788	2	E71813	probable component
255	71	5.9	913	2	T52485	neurofilament prot
256	71	5.9	2437	2	T18482	hypothetical prote
257	70.5	5.9	203	1	T31684	probable bacitraci
258	70.5	5.9	266	2	H98208	probable permease
259	70.5	5.9	266	2	A13077	hypothetical prote
260	70.5	5.9	266	2	T41414	probable receptor
261	70.5	5.9	279	2	AH2408	permease protein o
262	70.5	5.9	291	2	S22041	hypothetical prote
263	70.5	5.9	340	2	S76294	hypothetical prote
264	70.5	5.9	352	2	B90537	hypothetical prote
265	70.5	5.9	365	2	T18748	prostaglandin E re
266	70.5	5.9	365	2	S51315	prostaglandin E re
267	70.5	5.9	374	2	S18747	prostaglandin E re
268	70.5	5.9	374	2	S51317	prostaglandin E re
269	70.5	5.9	388	2	S51316	prostaglandin E re
270	70.5	5.9	388	2	T38750	prostaglandin recep
271	70.5	5.9	389	2	S71336	mesotocin receptor
272	70.5	5.9	390	2	S43375	prostaglandin E re
273	70.5	5.9	390	2	S51313	prostaglandin E re
274	70.5	5.9	393	2	S51318	prostaglandin E re
275	70.5	5.9	423	1	E71065	hypothetical prote
276	70.5	5.9	425	2	S51319	prostaglandin E re
277	70.5	5.9	426	2	AG3600	cellulose synthase
278	70.5	5.9	462	2	B64638	conserved hypochet
279	70.5	5.9	521	2	B64181	probable cytochrom
280	70.5	5.9	548	2	A81650	conserved hypochet
281	70.5	5.9	556	2	T16790	hypothetical prote
282	70.5	5.9	574	2	S45754	probable membrane
283	70.5	5.9	598	2	F46027	gamma-aminobutyric
284	70.5	5.9	599	1	ACR1CT	gamma-aminobutyric
285	70.5	5.9	700	2	T10566	probable serine/th
286	70.5	5.9	766	2	T48463	hypothetical prote
287	70.5	5.9	1026	2	T18220	chitin synthase (E
288	70.5	5.9	1583	2	F97846	hypothetical prote
289	70.5	5.9	1787	2	T20160	hypothetical prote
290	70.5	5.9	5138	2	B96695	hypothetical prote
291	70	5.9	189	2	T51847	manganese-binding
292	70	5.9	199	2	T08902	manganese-binding
293	70	5.9	213	2	F86310	protein P113.8 [lm
294	70	5.9	256	2	T13597	hypothetical prote
295	70	5.9	287	2	T52317	chlorophyll a/b-bi
296	70	5.9	292	2	H64244	H+-transporting tw
297	70	5.9	307	2	E95010	ABC transporter. p
298	70	5.9	307	2	B97882	hypothetical prote
299	70	5.9	330	2	T30981	hypothetical prote
300	70	5.9	333	2	T38974	G protein-coupled
301	70	5.9	371	2	T46421	hypothetical prote
302	70	5.9	388	2	A55597	oocytein receptor
303	70	5.9	416	2	A85112	hypothetical prote
304	70	5.9	418	2	T08882	probable ankyrin-r
305	70	5.9	420	2	E72357	proline/betaine tr
306	70	5.9	427	2	T01905	sugar ABC transpor
307	70	5.9	437	2	C91261	hypothetical prote
308	70	5.9	438	2	G86101	glutamate-aspartat
309	70	5.9	438	2	AP3215	glutamate-aspartat
310	70	5.9	450	2	T42595	ABC transporter. m
311	70	5.9	494	2	B89827	envelope protein 5
312	70	5.9	532	2	T49467	hypothetical prote
313	70	5.9	551	2	A87019	related to COP1-in
314	70	5.9	554	2	T27878	probable cytochrom
315	70	5.9	558	2	H72565	hypothetical prote
316	70	5.9	675	2	T22323	hypothetical prote
317	70	5.9	735	2	S46830	urea transport pro
318	70	5.9	963	2	T26022	hypothetical prote
319	70	5.9	1930	2	F86200	protein P12X1.17
320	69.5	5.8	133	1	MMIHC	nonstructural prot
321	69.5	5.8	206	2	S76279	hypothetical prote
322	69.5	5.8	322	2	F70194	hypothetical prote
323	69.5	5.8	323	2	S59388	probable membrane
324	69.5	5.8	324	2	A97736	hypothetical prote
325	69.5	5.8	325	2	G90444	hypothetical prote
326	69.5	5.8	326	2	I58186	probable G protein
327	69.5	5.8	327	2	A53216	prostaglandin E2 r
328	69.5	5.8	328	2	S36766	prostaglandin E re
329	69.5	5.8	329	2	S62758	ubiquinol-cytochro
330	69.5	5.8	330	2	S36765	prostaglandin E re
331	69.5	5.8	331	2	S36767	prostaglandin E re
332	69.5	5.8	332	2	T32561	prostaglandin E re
333	69.5	5.8	333	2	A91208	cell-division prot
334	69.5	5.8	334	2	S51791	Drosophila translo
335	69.5	5.8	335	2	E90986	probable colanic a
336	69.5	5.8	336	2	H85831	probable colanic a
337	69.5	5.8	337	2	G64971	putative colanic a
338	69.5	5.8	338	2	B53216	prostaglandin E2 r
339	69.5	5.8	339	2	S36764	prostaglandin E re
340	69.5	5.8	340	2	G72300	conserved hypochet
341	69.5	5.8	341	2	T44832	probable emulsan r
342	69.5	5.8	342	2	D98003	conserved hypochet
343	69.5	5.8	343	2	T25798	hypothetical prote
344	69.5	5.8	344	2	E82740	C4-dicarboxylate t
345	69.5	5.8	345	2	C86250	hypothetical prote
346	69.5	5.8	346	2	T50054	probable transpor
347	69.5	5.8	347	2	E86534	ADP/ATP translocas
348	69.5	5.8	348	2	G86581	integral membrane
349	69.5	5.8	349	2	F72042	integral membrane
350	69.5	5.8	350	2	UW0089	organic cation tra
351	69.5	5.8	351	2	AC2137	ABC transporter AT
352	69.5	5.8	352	2	B96776	hypothetical prote
353	69.5	5.8	353	2	D97337	mismatch repair pr
354	69.5	5.8	354	2	AG1412	DNA polymerase III
355	69.5	5.8	355	2	AF1788	DNA polymerase III
356	69.5	5.8	356	2	S11073	gamma-aminobutyric
357	69.5	5.8	357	2	T31042	hypothetical prote
358	69.5	5.8	358	2	F84525	Mutator-like trans
359	69.5	5.8	359	2	E84463	Mutator-like trans
360	69.5	5.8	360	2	S58824	probable membrane
361	69.5	5.8	361	2	S46633	probable membrane
362	69.5	5.8	362	2	A59188	ATP-binding casaset
363	69.5	5.8	363	2	S71363	probable ATP-bind1
364	69.5	5.8	364	2	UT0382	apolipoprotein B -
365	69.5	5.8	365	2	T16569	hypothetical prote
366	69.5	5.8	366	2	T15789	hypothetical prote
367	69.5	5.8	367	2	E83941	hypothetical prote
368	69	5.8	368	2	A96998	CDP-diglyceride sy
369	69	5.8	369	2	H96934	uncharacterized me
370	69	5.8	370	2	G64145	hypothetical prote
371	69	5.8	371	2	T07481	hypothetical prote
372	69	5.8	372	2	F83805	hypothetical prote
373	69	5.8	373	2	C71707	hypothetical prote
374	69	5.8	374	2	S72554	melatonin receptor
375	69	5.8	375	2	D96002	probable sugar upt
376	69	5.8	376	2	T32702	hypothetical prote
377	69	5.8	377	2	A99979	hypothetical prote
378	69	5.8	378	2	B69436	LSU ribosomal prot
379	69	5.8	379	2	AH1514	hypothetical prote
380	69	5.8	380	2	AD0273	probable integral
381	69	5.8	381	2	S58447	ubiquinol-cytochro
382	69	5.8	382	2	A13175	conserved hypochet
383	69	5.8	383	2	D71424	hypothetical prote
384	69	5.8	384	2	T69644	O-antigen polymera
385	69	5.8	385	2	T11268	NADH2 dehydrogenas
386	69	5.8	386	2	A42384	glutamate-aspartat
387	69	5.8	387	2	T19512	hypothetical prote
388	69	5.8	388	2	S25821	transposase - Bac1
389	69	5.8	389	2	T33985	hypothetical prote
390	69	5.8	390	2	E96804	probable thioredox
391	69	5.8	391	2	T11916	NADH2 dehydrogenas
392	69	5.8	392	2	T24675	hypothetical prote
393	69	5.8	393	2	E70784	cytochrome b homol
394	69	5.8	394	2	A64100	inner membrane cop

395	69	5.8	599	2	G90476	probable Na <sup>+</sup> /H <sup>+</sup> an	468	68	5.7	426	2	C69831	conserved hypothet
396	69	5.8	600	2	T11889	NADH2 dehydrogenas	469	68	5.7	473	2	C70414	NADH2 dehydrogenas
397	69	5.8	637	2	H96592	probable multigan	470	68	5.7	474	2	H71044	hypothetical prote
398	69	5.8	659	2	D84633	probable multigan	471	68	5.7	475	2	E83450	cytochrome-c oxida
399	69	5.8	791	2	T12455	hypothetical prote	472	68	5.7	477	2	H91123	probable oxidoredu
400	69	5.8	802	2	JH0595	potassium channel	473	68	5.7	477	2	G85968	probable oxidoredu
401	69	5.8	863	2	H84490	hypothetical prote	474	68	5.7	477	2	C65096	hypothetical 52.1
402	69	5.8	933	2	AD3309	hypothetical membr	475	68	5.7	488	2	A53572	prostaglandin 52 r
403	69	5.8	1058	2	T30580	P-type ATPase - s1	476	68	5.7	502	1	I30010	NADH2 dehydrogenas
404	69	5.8	1344	2	T34188	myb-binding protei	477	68	5.7	519	2	T39918	probable acetyl-co
405	69	5.8	1392	2	T01908	hypothetical prote	478	68	5.7	542	2	A69261	probable acid-CoA
406	69	5.8	1515	2	T04204	hypothetical prote	479	68	5.7	542	2	B81910	probable ABC-trans
407	69	5.8	3010	1	A45573	genome polypept	480	68	5.7	542	2	B81105	ABC transporter, A
408	69	5.7	225	2	AE0371	probable carboxype	481	68	5.7	620	2	T11907	hypothetical prote
409	69	5.7	237	2	T25877	hypothetical prote	482	68	5.7	664	2	C84869	probable receptor
410	69	5.7	238	2	T04280	hypothetical prote	483	68	5.7	718	2	E83718	hypothetical prote
411	69	5.7	260	2	H75428	hypothetical prote	484	68	5.7	804	2	T49975	hypothetical prote
412	69	5.7	262	2	AG1830	hypothetical prote	485	68	5.7	836	2	T18460	hypothetical prote
413	69	5.7	265	2	A13428	O-antigen export s	486	68	5.7	859	2	S69700	hypothetical prote
414	69	5.7	285	2	E86835	maltoase export s	487	68	5.7	871	2	H72597	hypothetical prote
415	69	5.7	297	2	S74335	carbon dioxide con	488	68	5.7	1429	2	T19422	hypothetical prote
416	69	5.7	304	2	AG3035	hypothetical prote	489	68	5.7	1878	2	E86189	hypothetical prote
417	69	5.7	304	2	D98250	probable sugar ABC	490	68	5.7	3010	1	GNMYTC	genome polypept
418	69	5.7	343	2	AC2129	iron(III) dicitrat	491	68	5.7	104	2	T36801	hypothetical prote
419	69	5.7	359	2	B59105	hypothetical prote	492	68	5.7	200	2	H72295	conserved hypothet
420	69	5.7	362	2	D72424	oligopeptide ABC t	493	68	5.7	273	2	A97700	hypothetical prote
421	69	5.7	377	1	J02337	omega-3 fatty acid	494	68	5.7	288	2	F72219	conserved hypothet
422	69	5.7	383	2	I53870	Bdg-1 orphan recep	495	68	5.7	320	2	T23674	hypothetical prote
423	69	5.7	391	2	H81265	probable transmem	496	68	5.7	323	1	Q08BD3	HRF3 protein - hu
424	69	5.7	395	2	B83774	hypothetical prote	497	68	5.7	348	2	T12591	NADH2 dehydrogenas
425	69	5.7	395	2	B83774	hypothetical prote	498	68	5.7	354	2	T09353	G protein-coupled
426	69	5.7	395	2	A96189	conserved hypothet	499	68	5.7	362	2	C88086	protein T11P1.1 [i
427	69	5.7	419	2	AG1660	multidrug resistan	500	68	5.7	387	2	T24581	hypothetical prote
428	69	5.7	420	2	I51666	Mel-1c receptor su	501	68	5.7	397	2	A81399	mutants block spor
429	69	5.7	425	2	F97108	probable glycosylt	502	68	5.7	419	2	AH1288	multidrug resistan
430	69	5.7	430	2	S15308	hypothetical prote	503	68	5.7	439	2	H83599	sodium-dependent c
431	69	5.7	431	2	H72247	preproteins translo	504	68	5.7	450	2	G91219	TDP-FucNAc lipidi
432	69	5.7	444	2	A48260	corticoidlberin rec	505	68	5.7	450	2	A86066	TDP-FucNAc lipidi
433	69	5.7	445	2	E22845	hypothetical prote	506	68	5.7	450	2	F65183	4-alpha-1-fucosylt
434	69	5.7	479	2	T44326	hypothetical prote	507	68	5.7	452	2	G89870	hypothetical prote
435	69	5.7	480	2	E70446	hypothetical prote	508	68	5.7	459	2	JH0594	vasoactive intesti
436	69	5.7	488	2	T15941	hypothetical prote	509	68	5.7	483	2	G84113	hypothetical prote
437	69	5.7	492	2	G90574	NADH2 dehydrogenas	510	68	5.7	488	1	QXASM4	NADH2 dehydrogenas
438	69	5.7	502	2	S77331	probable cyclochrom	511	68	5.7	492	2	F64464	sodium-dependent n
439	69	5.7	512	2	T00605	probable cyclochrom	512	68	5.7	498	2	T48262	hypothetical prote
440	69	5.7	518	2	S50465	PgC2 protein - Yea	513	68	5.7	515	2	E72089	ADP, ATP carrier p
441	69	5.7	525	2	JN0902	pituitary adenylat	514	68	5.7	516	2	H82973	choline transpor
442	69	5.7	542	2	S58102	hypothetical prote	515	68	5.7	566	2	I51368	gamma-aminobutyric
443	69	5.7	558	2	F64235	Na <sup>+</sup> ATPase chain J	516	68	5.7	632	2	A71259	probable dicarboxy
444	69	5.7	634	2	C83530	potassium uptake p	517	68	5.7	676	1	WZV218	18 protein - vaccl
445	69	5.7	670	2	G86702	unknown protein [i	518	68	5.7	676	2	T37345	NPH-II, helicase -
446	69	5.7	724	2	H86427	cation-transportin	519	68	5.7	676	2	D42511	18R protein - vacc
447	69	5.7	788	2	G64707	probable membrane	520	68	5.7	676	2	F36843	ATP/GTP-binding pr
448	69	5.7	923	1	MMBY7C	probable copper-tr	521	68	5.7	676	2	T28500	hypothetical prote
449	69	5.7	1004	1	S55353	hypothetical prote	522	68	5.7	682	2	D72158	18R protein - vari
450	69	5.7	146	2	H75201	hypothetical prote	523	68	5.7	686	2	G82448	sensor histidine k
451	69	5.7	205	2	A64373	hypothetical prote	524	68	5.7	716	2	S30687	hypothetical prote
452	69	5.7	255	2	F39925	hypothetical prote	525	68	5.7	740	1	T02567	probable ATP-bindi
453	69	5.7	266	2	C95316	probable ABC trans	526	68	5.7	866	2	A54163	vacuolar ATPase (E
454	69	5.7	270	2	AE3627	maltoase transport	527	68	5.7	866	2	T20574	hypothetical prote
455	69	5.7	279	2	AG2165	bicarbonate transp	528	68	5.7	950	2	T15915	hypothetical prote
456	69	5.7	294	2	T41953	G protein-coupled	529	68	5.7	1159	2	T02866	hypothetical prote
457	69	5.7	294	2	AE0004	ribonuclease BN (E	530	68	5.7	1244	2	T19615	hypothetical prote
458	69	5.7	313	2	B38888	COI intion 9 prote	531	68	5.7	1411	2	S48442	PDRL1 protein - ye
459	69	5.7	355	2	A45177	chemokine (C-C) re	532	68	5.7	1753	2	S30855	hypothetical prote
460	69	5.7	360	2	T11067	ubiquinol-cytochro	533	68	5.7	2332	1	GNMYF	genome polypept
461	69	5.7	364	2	UC2115	prostaglandin E re	534	68	5.7	151	2	A72093	conserved hypothet
462	69	5.7	365	2	JN0693	prostaglandin E2 r	535	68	5.7	151	2	H86529	CT101 hypothetical
463	69	5.7	370	2	H90559	hypothetical prote	536	68	5.7	159	2	S61040	probable membrane
464	69	5.7	379	2	S58450	ubiquinol-cytochro	537	68	5.7	180	2	T49129	kel69 (escapes X-1
465	69	5.7	393	2	AG0184	probable multidrug	538	68	5.7	203	2	D70150	hypothetical glycop
466	69	5.7	402	2	T41253	hypothetical wctis	539	68	5.7	225	1	MMTHIB	El membrane glycop
467	69	5.7	417	2	T11387	NADH2 dehydrogenas	540	68	5.7	244	2	D70404	conserved hypothet



541	67	5.6	255	2	C90078	hypothetical prote
542	67	5.6	275	2	G98194	sugar ABC transpor
543	67	5.6	275	2	AC3082	hypothetical prote
544	67	5.6	275	2	575698	hypothetical prote
545	67	5.6	276	2	669307	conserved hypothet
546	67	5.6	276	2	S35270	DNA-damage repair
547	67	5.6	283	2	P96959	rRNA-processing ri
548	67	5.6	285	2	AE1024	hypothetical prote
549	67	5.6	286	2	D64235	hypothetical prote
550	67	5.6	314	2	D96703	hypothetical prote
551	67	5.6	317	2	D98260	inner membrane pro
552	67	5.6	336	2	A96997	ferrichrome transp
553	67	5.6	345	2	T21776	hypothetical prote
554	67	5.6	349	2	D84166	hypothetical prote
555	67	5.6	350	2	C88987	protein C50H11.2
556	67	5.6	352	2	T32314	hypothetical prote
557	67	5.6	379	2	S58451	ubiquinol-cytochro
558	67	5.6	379	2	S58449	ubiquinol-cytochro
559	67	5.6	396	1	C69291	phenomone shutdow
560	67	5.6	407	2	E70309	hypothetical prote
561	67	5.6	411	2	E71500	probable amino aci
562	67	5.6	415	2	S74041	pyruvate synthase
563	67	5.6	416	2	T46401	hypothetical prote
564	67	5.6	423	2	C95085	sodium-dependent c
565	67	5.6	436	2	AC1021	proton glutamate s
566	67	5.6	441	2	P86279	hypothetical prote
567	67	5.6	446	2	G72287	hypothetical prote
568	67	5.6	446	2	A31986	glucose transpor
569	67	5.6	507	2	AB1707	glycine betaine tr
570	67	5.6	516	2	AB0665	probable membrane
571	67	5.6	646	2	T37777	AMP binding casnet
572	67	5.6	717	2	T49238	hypothetical prote
573	67	5.6	753	2	S58331	dolichyl-phosphate
574	67	5.6	769	2	F81415	DNA topoisomerase
575	67	5.6	784	2	C82679	cell division prot
576	67	5.6	787	2	PN0677	hypothetical prote
577	67	5.6	798	2	T34248	hypothetical prote
578	67	5.6	814	2	T05537	probable serine/th
579	67	5.6	823	2	T35280	probable integral
580	67	5.6	880	2	D69427	conserved hypothet
581	67	5.6	891	2	B82495	probable NADH dehy
582	67	5.6	900	2	E66631	galactosamine-cont
583	67	5.6	1175	2	S39951	chitin synthase (E
584	67	5.6	1242	1	D3B8C1	DNA-directed DNA p
585	67	5.6	1333	2	S63403	probable membrane
586	67	5.6	1511	2	A53151	pleiotropic drug r
587	67	5.6	1575	2	G82905	conserved hypothet
588	67	5.6	1879	2	T19481	hypothetical prote
589	67	5.6	1905	2	T18267	multidrug resistan
590	67	5.6	1993	2	T30982	sodium channel SCA
591	67	5.6	3010	1	GMWVC3	genome polyproteic
592	67	5.6	153	1	G69847	conserved hypothet
593	67	5.6	203	2	T28732	hypothetical prote
594	67	5.6	204	2	C70506	hypothetical prote
595	67	5.6	218	2	C64586	cag pathogenicity
596	67	5.6	245	2	A81405	sec-independent pr
597	67	5.6	263	2	A12384	hypothetical prote
598	67	5.6	268	2	A70417	hypothetical prote
599	67	5.6	272	2	A10075	probable permease
600	67	5.6	279	1	S56642	nitrate transpor
601	67	5.6	279	1	E70322	hypothetical prote
602	67	5.6	293	2	A84110	sugar ABC transpor
603	67	5.6	294	2	S70876	hypothetical prote
604	67	5.6	316	2	F81712	ABC transporter, p
605	67	5.6	333	2	S77103	hypothetical prote
606	67	5.6	347	2	AD2201	hypothetical prote
607	67	5.6	356	2	T20737	hypothetical prote
608	67	5.6	359	2	P90055	conserved hypothet
609	67	5.6	367	2	S75936	hypothetical prote
610	67	5.6	380	2	G89786	hypothetical prote
611	67	5.6	384	1	I38890	dial specificity p
612	67	5.6	389	2	E96516	Fltn3.13 [imported
613	67	5.6	400	2	G00013	D3 dopamine recept
614	67	66.5	614	2	G89773	hypothetical prote
615	67	66.5	615	2	H95041	polyaccharide tra
616	67	66.5	616	2	D98111	hypothetical prote
617	67	66.5	617	2	G95246	maltodextrin ABC t
618	67	66.5	618	2	B95135	MATE efflux family
619	67	66.5	619	2	H71228	hypothetical prote
620	67	66.5	620	2	G71969	cytochrome-c oxida
621	67	66.5	621	2	D84998	low-affinity inorg
622	67	66.5	622	2	A46391	CAMP receptor sub
623	67	66.5	623	2	AC1555	efflux transporter
624	67	66.5	624	2	A71875	hypothetical prote
625	67	66.5	625	2	T32644	hypothetical prote
626	67	66.5	626	2	T27627	hypothetical prote
627	67	66.5	627	2	G83720	nickel transport s
628	67	66.5	628	2	E91135	probable alkaline
629	67	66.5	629	2	H85380	probable alkaline
630	67	66.5	630	2	A48026	sterol O-acetyltras
631	67	66.5	631	2	C71424	hypothetical prote
632	67	66.5	632	2	A11510	C-terminal domain
633	67	66.5	633	2	T32430	hypothetical prote
634	67	66.5	634	2	AG2596	cytochrome c-type
635	67	66.5	635	2	G97478	cytochrome c-type
636	67	66.5	636	2	I56506	Na+/Cl(-)-depend
637	67	66.5	637	2	S27043	neurotransmitter t
638	67	66.5	638	2	S19876	genome polyproteic
639	67	66.5	639	2	B36786	hypothetical prote
640	67	66.5	640	2	T47311	hypothetical prote
641	67	66.5	641	2	T27479	hypothetical prote
642	67	66.5	642	2	T31433	Na+/Ca2+,K+-exchan
643	67	66.5	643	2	C88854	protein FlhA10.3
644	67	66.5	644	2	H81037	DNA polymerase III
645	67	66.5	645	2	T15961	hypothetical prote
646	67	66.5	646	2	JW0057	gravin human
647	67	66.5	647	2	E85062	hypothetical prote
648	67	66.5	648	2	S16449	genome polyproteic
649	67	66.5	649	2	G02434	DNA-directed DNA p
650	67	66.5	650	2	A43360	inositol 1,4,5-tri
651	67	66.5	651	1	GMWVC3	genome polyproteic
652	67	66.5	652	2	S28759	NADH2 dehydrogenas
653	67	66.5	653	2	D83620	diacylglycerol kin
654	67	66.5	654	2	A89801	conserved hypothet
655	67	66.5	655	2	H96816	hypothetical prote
656	67	66.5	656	2	S42125	hypothetical prote
657	67	66.5	657	2	D87447	sulfate ABC transp
658	67	66.5	658	2	A99074	hypothetical prote
659	67	66.5	659	2	I47040	sterol O-acetyltras
660	67	66.5	660	2	B41671	iron transport pro
661	67	66.5	661	2	B84291	hypothetical prote
662	67	66.5	662	2	E71137	hypothetical prote
663	67	66.5	663	2	C97272	hypothetical prote
664	67	66.5	664	2	S52315	conserved membrane
665	67	66.5	665	2	I52315	G protein-coupled
666	67	66.5	666	2	S17405	ubiquinol-cytochro
667	67	66.5	667	2	S17409	ubiquinol-cytochro
668	67	66.5	668	2	S58460	ubiquinol-cytochro
669	67	66.5	669	2	A35300	G protein-coupled
670	67	66.5	670	2	QO8RT9	protein U133 - hum
671	67	66.5	671	2	T21154	hypothetical prote
672	67	66.5	672	2	T44477	hypothetical prote
673	67	66.5	673	2	B70505	hypothetical prote
674	67	66.5	674	2	T44831	probable emulsan r
675	67	66.5	675	2	B64927	probable sugar tra
676	67	66.5	676	2	A85777	probable transport
677	67	66.5	677	2	E90928	probable transport
678	67	66.5	678	2	H86539	CBS domain protein
679	67	66.5	679	2	A82444	Gedfer family prote
680	67	66.5	680	2	T41027	hypothetical wfc5
681	67	66.5	681	2	B72363	hypothetical prote
682	67	66.5	682	2	T07366	probable phosphat
683	67	66.5	683	2	T14816	hypothetical prote
684	67	66.5	684	2	T18633	hypothetical prote
685	67	66.5	685	2	A37223	alpha-2b-adreneryl
686	67	66.5	686	2	A38316	alpha-2-adreneryic
687	67	66.5	687	2	F86846	ABC transporter pe

687	66	5.5	483	2	S75369	hypothetical prote	760	65.5	5.5	561	2	S71189	Dwarf1 protein - A
688	66	5.5	484	2	T24238	hypothetical prote	761	65.5	5.5	575	2	AH1417	ABC transporter (A
689	66	5.5	486	2	B82940	hypothetical prote	762	65.5	5.5	578	2	T15736	hypothetical prote
690	66	5.5	508	2	C47677	hypothetical prote	763	65.5	5.5	583	2	AH1151	glycerophosphoryl
691	66	5.5	525	2	T28306	ORF MSV145 hypothe	764	65.5	5.5	590	2	C81316	probable sugar epi
692	66	5.5	527	2	G69635	PTS arbutin-like e	765	65.5	5.5	597	2	B82881	hypothetical prote
693	66	5.5	532	2	A90037	hypothetical prote	766	65.5	5.5	618	2	AB1167	phosphotransferase
694	66	5.5	546	2	A69890	hypothetical prote	767	65.5	5.5	617	2	AC1204	phosphotransferase
695	66	5.5	548	2	B87423	cytochrome-c oxida	768	65.5	5.5	642	2	H70331	ATP-dependent heli
696	66	5.5	552	2	S45886	hypothetical prote	769	65.5	5.5	718	2	A56851	Na+/myo-inositol c
697	66	5.5	565	2	S73707	Na(+) translocatin	770	65.5	5.5	720	2	H82198	RTX toxin transpor
698	66	5.5	570	2	S07744	NMDH2 dehydrogenas	771	65.5	5.5	721	2	AF1254	penicillin-binding
699	66	5.5	573	1	S33212	INDM1 protein - fu	772	65.5	5.5	740	2	S61568	probable membrane
700	66	5.5	573	2	AP1418	ABC transporter, A	773	65.5	5.5	860	1	QRHULD	IDL receptor precu
701	66	5.5	573	2	AH1793	ABC transporter, A	774	65.5	5.5	958	2	AC0204	cellulose 1,4-beta
702	66	5.5	619	2	T11314	NMDH2 dehydrogenas	775	65.5	5.5	1087	1	S41797	TYB protein - yea
703	66	5.5	632	2	T24405	hypothetical prote	776	65.5	5.5	1328	2	B22999	SRB8 protein - yea
704	66	5.5	654	2	A98350	hypothetical ABC t	777	65.5	5.5	1427	2	S74293	hypothetical prote
705	66	5.5	654	2	AF2932	hypothetical prote	778	65.5	5.5	1581	2	B71636	hypothetical prote
706	66	5.5	705	2	T48464	hypothetical prote	779	65.5	5.5	1635	2	T32452	probable membrane
707	66	5.5	721	2	A70764	probable glxg prot	780	65.5	5.4	126	2	AD0340	transcription regu
708	66	5.5	736	2	G01522	acidic 82 kDa prot	781	65	5.4	149	2	C69393	early K1B 21k prot
709	66	5.5	784	2	B90442	tricorn proteinase	782	65	5.4	176	1	Q1AD25	hypothetical prote
710	66	5.5	1039	2	S76747	hypothetical prote	783	65	5.4	136	2	S40728	B1 membrane glycop
711	66	5.5	1054	2	A61221	probable calcium t	784	65	5.4	225	1	MMHIV	serotonin receptor
712	66	5.5	1359	2	T34036	hypothetical prote	785	65.5	5.4	247	2	I48149	hypothetical prote
713	66	5.5	1375	2	S48375	hypothetical prote	786	65	5.4	257	2	B75099	growth response pr
714	66	5.5	2599	2	P90608	ABC transporter pe	787	65	5.4	259	2	A47112	hema concentration
715	66	5.5	26926	1	I38344	titin, cardiac mus	788	65	5.4	271	2	B8950	nitrate transport
716	65.5	5.5	132	2	B97760	NMDH2 dehydrogenas	789	65	5.4	280	2	S75957	probable chlorophy
717	65.5	5.5	132	2	B70074	hypothetical prote	790	65	5.4	290	2	T02877	cytochrome c oxida
718	65.5	5.5	146	2	G69447	hypothetical prote	791	65	5.4	291	2	C97453	cytochrome c oxida
719	65.5	5.5	171	2	A13476	signal peptidase I	792	65	5.4	307	2	AB2671	branched-chain ami
720	65.5	5.5	197	2	T17106	hypothetical prote	793	65	5.4	313	2	B36125	lysophospholipase
721	65.5	5.5	210	2	S67771	endoplasmic reticu	794	65	5.4	344	2	AD1200	hypothetical prote
722	65.5	5.5	252	2	T43100	signal sequence pe	795	65	5.4	339	2	D87087	hypothetical prote
723	65.5	5.5	290	2	G69456	phosphate ABC tran	796	65	5.4	322	2	S38091	dipeptide abc tran
724	65.5	5.5	297	2	B86839	hypothetical prote	797	65	5.4	330	2	H75068	hypothetical prote
725	65.5	5.5	297	2	F83792	hypothetical prote	798	65	5.4	335	2	H75029	NMDH2 dehydrogenas
726	65.5	5.5	301	2	T21308	polyulfide reduct	799	65	5.4	338	2	S50339	conserved hypochet
727	65.5	5.5	317	2	S23459	probable binding p	800	65	5.4	344	2	AD1200	NMDH2 dehydrogenas
728	65.5	5.5	327	2	T36087	NMDH2 dehydrogenas	801	65	5.4	345	2	T12361	hypothetical prote
729	65.5	5.5	348	1	S36003	hypothetical ferrit	802	65	5.4	355	2	G70200	hypothetical prote
730	65.5	5.5	351	2	F82880	spore germination	803	65	5.4	359	2	T15249	mannan endo-1,4-be
731	65.5	5.5	365	1	F69629	prostaglandin R2 r	804	65	5.4	362	2	H69785	ubiquinol-cytochro
732	65.5	5.5	367	2	JC2056	ubiquinol-cytochro	805	65	5.4	375	2	I38879	ubiquinol-cytochro
733	65.5	5.5	379	2	S58456	hypothetical prote	806	65	5.4	379	1	S17414	ubiquinol-cytochro
734	65.5	5.5	379	2	T32778	hypothetical prote	807	65	5.4	379	2	S58461	ubiquinol-cytochro
735	65.5	5.5	391	2	T32601	nucleoside permeas	808	65	5.4	379	2	S58455	ubiquinol-cytochro
736	65.5	5.5	394	2	AH0362	NMDH2 dehydrogenas	809	65	5.4	380	1	D34285	ubiquinol-cytochro
737	65.5	5.5	410	2	T11064	conserved hypochet	810	65	5.4	382	2	T11138	hypothetical prote
738	65.5	5.5	423	2	A97688	hypothetical 45.5K	811	65	5.4	390	2	C84984	hypothetical prote
739	65.5	5.5	425	2	AF2913	conserved hypochet	812	65	5.4	415	2	T21532	hypothetical prote
740	65.5	5.5	425	2	AF2913	conserved hypochet	813	65	5.4	438	2	B81410	probable integral
741	65.5	5.5	429	2	T32832	microfibril-associ	814	65	5.4	442	2	A83122	probable MFS trans
742	65.5	5.5	442	2	A42670	probable transcrip	815	65	5.4	445	2	AD2358	glucosyltransferas
743	65.5	5.5	445	2	T38916	probable dicarboxy	816	65	5.4	457	2	T28334	Ser/Thr protein ki
744	65.5	5.5	449	2	H83629	hypothetical prote	817	65	5.4	462	2	B88613	protein T27B9.5 [1
745	65.5	5.5	457	2	A75327	hypothetical prote	818	65	5.4	479	2	S54508	TRK system potassi
746	65.5	5.5	477	2	B75170	hypothetical prote	819	65	5.4	479	2	A69036	cytochrome-c oxida
747	65.5	5.5	480	2	A60043	endoplasmic reticu	820	65	5.4	481	2	B81050	probable sugar tra
748	65.5	5.5	487	2	A97928	type I site-specif	821	65	5.4	490	2	T14545	NMDH2 dehydrogenas
749	65.5	5.5	488	1	H64537	cytochrome-c oxida	822	65	5.4	492	2	S59107	hypothetical prote
750	65.5	5.5	491	2	G81295	cytochrome-c oxida	823	65	5.4	510	2	S55204	polyaccharide bio
751	65.5	5.5	491	2	AE1197	efflux transporter	824	65	5.4	511	2	H75097	probable membrane
752	65.5	5.5	495	2	A97022	probably membrane	825	65	5.4	513	2	T37180	hydrolase 4 memb
753	65.5	5.5	500	2	G84706	hypothetical prote	826	65	5.4	526	2	D91047	hypothetical prote
754	65.5	5.5	502	2	AD3395	NMDH2 dehydrogenas	827	65	5.4	530	2	B89771	conserved hypochet
755	65.5	5.5	502	2	T25669	hypothetical prote	828	65	5.4	535	2	A64697	hypothetical prote
756	65.5	5.5	518	2	A53207	probable folate tr	829	65	5.4	539	2	S55190	hypothetical prote
757	65.5	5.5	528	2	T34417	delayed rectifier	830	65	5.4	547	2	T31543	SMG1 protein yea
758	65.5	5.5	544	2	B84825	probable ABC trans	831	65	5.4	547	2	S53920	hypothetical prote
759	65.5	5.5	545	2	B90460	hypothetical prote	832	65	5.4	576	2	T25375	hypothetical prote

833	65	5.4	579	2	S61131	probable membrane
834	65	5.4	608	2	S65298	dicarboxylic amino
835	65	5.4	611	2	T21747	hypothetical prote
836	65	5.4	624	2	G82508	hypothetical prote
837	65	5.4	627	2	T11125	NMDH2 dehydrogenas
838	65	5.4	633	2	F84483	mutator-like trans
839	65	5.4	638	2	D69957	conserved hypothet
840	65	5.4	643	2	P97787	sodium/pantothenat
841	65	5.4	676	2	A45515	diak-type molecula
842	65	5.4	684	2	F86394	protein T24P13.20
843	65	5.4	697	2	H84791	hypothetical prote
844	65	5.4	702	2	T13505	NMDH2 dehydrogenas
845	65	5.4	705	2	T04400	NMDH2 dehydrogenas
846	65	5.4	773	2	H96818	hypothetical prote
847	65	5.4	773	2	G83816	late competence op
848	65	5.4	808	2	T04459	hypothetical prote
849	65	5.4	861	2	S77086	hypothetical prote
850	65	5.4	927	2	T38518	ribonuclease II RN
851	65	5.4	931	2	F84637	probable plasma me
852	65	5.4	938	2	T01809	hypothetical prote
853	65	5.4	1089	2	C70522	probable mmp18 pro
854	65	5.4	1163	2	D64315	type I restriction
855	65	5.4	1178	2	S76370	sensory transducti
856	65	5.4	1232	2	I38496	anion exchanger 3
857	65	5.4	1421	2	T34225	hypothetical prote
858	65	5.4	5069	2	T17464	rifamycin polypept
859	65	5.4	180	2	T41339	hypothetical prote
860	65	5.4	211	2	S35280	eac protein - phag
861	65	5.4	217	2	AE0395	probable amino aci
862	65	5.4	227	2	C69432	hypothetical prote
863	65	5.4	234	2	E96957	NAD superfamily hy
864	65	5.4	268	2	AF2470	potassium channel
865	65	5.4	271	2	B81894	proliporotein dia
866	65	5.4	275	2	T43119	hypothetical prote
867	65	5.4	293	2	D71517	probable metal tra
868	65	5.4	295	2	T32202	hypothetical prote
869	65	5.4	297	2	T27584	hypothetical prote
870	65	5.4	320	2	T23904	hypothetical prote
871	65	5.4	326	2	A86411	protein P3M18.6 [i
872	65	5.4	353	2	F64175	hypothetical prote
873	65	5.4	358	2	T22823	hypothetical prote
874	65	5.4	361	2	A86841	hypothetical prote
875	65	5.4	361	2	A40734	Pas (Pasover) pro
876	65	5.4	379	2	S43264	ubiquitinol-cytochro
877	65	5.4	379	2	T11505	ubiquitinol-cytochro
878	65	5.4	379	2	S58454	ubiquitinol-cytochro
879	65	5.4	379	2	A53077	ubiquitinol-cytochro
880	65	5.4	381	1	CBMS	pituitary adenylat
881	65	5.4	381	2	S33449	hypothetical prote
882	65	5.4	385	2	H69154	phosphoglycerate k
883	65	5.4	398	2	H95057	phosphoglycerate k
884	65	5.4	398	2	A97927	d3 dopamine recept
885	65	5.4	400	2	G01977	LAG1 protein - Yea
886	65	5.4	411	2	S46800	rod shape-determin
887	65	5.4	416	2	AF1127	UMP-N-acetylglucos
888	65	5.4	426	2	T45800	NMDH2 dehydrogenas
889	65	5.4	435	2	T11162	probable maltodext
890	65	5.4	435	2	AC0105	NMDH2 dehydrogenas
891	65	5.4	439	2	C22845	hypothetical prote
892	65	5.4	439	2	A84153	hypothetical prote
893	65	5.4	443	2	B26696	NMDH2 dehydrogenas
894	65	5.4	444	2	T11474	P44 hepatitis-aabo
895	65	5.4	444	2	A13676	microtubular aggre
896	65	5.4	444	2	S48218	dopamine receptor
897	65	5.4	446	1	D85362	hypothetical prote
898	65	5.4	448	2	S57909	probable histidine
899	65	5.4	448	2	T23528	hypothetical prote
900	65	5.4	450	2	D70045	two-component sens
901	65	5.4	451	2	UN0616	pituitary adenylat
902	65	5.4	467	2	C29051	transposase C - Ba
903	65	5.4	478	2	FMSYG2	glycinin chain Ala
904	65	5.4	495	1	S10851	glycinin G1 precur
905	65	5.4	495	2	S10851	
906	64.5	5.4	906	2	S39061	pituitary adenylat
907	64.5	5.4	907	2	S36114	pituitary adenylat
908	64.5	5.4	908	2	H64664	probable membrane
909	64.5	5.4	909	2	A99549	amino acid permeas
910	64.5	5.4	910	2	S39060	pituitary adenylat
911	64.5	5.4	911	2	H65107	hypothetical 61.6
912	64.5	5.4	912	2	A56730	carl protein - Pod
913	64.5	5.4	913	2	B97812	virulence factor m
914	64.5	5.4	914	2	AB1793	ABC transporter (A
915	64.5	5.4	915	2	T05304	cytochrome P450 97
916	64.5	5.4	916	2	B89869	hypothetical prote
917	64.5	5.4	917	2	AC1236	acyltansferase b14
918	64.5	5.4	918	2	COBY2M	mRNA maturase b14
919	64.5	5.4	919	2	T26307	hypothetical prote
920	64.5	5.4	920	2	T47648	ABC transporter-11
921	64.5	5.4	921	2	AD1617	penicillin-binding
922	64.5	5.4	922	2	AE1491	hypothetical prote
923	64.5	5.4	923	2	AD0341	probable membrane
924	64.5	5.4	924	2	AD1070	phosphatidylglycer
925	64.5	5.4	925	2	A89862	Na+/H+ antiporter
926	64.5	5.4	926	2	H64568	histidine kinase -
927	64.5	5.4	927	2	T30715	probable major cor
928	64.5	5.4	928	2	A70848	probable membrane
929	64.5	5.4	929	2	JC8066	138K protein - Tet
930	64.5	5.4	930	2	UH0284	125K surface antiq
931	64.5	5.4	931	2	B70723	probable mmp12 pr
932	64.5	5.4	932	2	T48829	related to SRBP c
933	64.5	5.4	933	2	S45628	DNA-directed DNA p
934	64.5	5.4	934	2	S69688	hypothetical prote
935	64.5	5.4	935	2	S64403	BSPI protein - Yea
936	64.5	5.4	936	2	S64800	probable membrane
937	64.5	5.4	937	1	GNWVJ8	genome polyprotein
938	64	5.4	938	2	A70041	conserved hypothet
939	64	5.4	939	2	G82359	conserved hypothet
940	64	5.4	940	2	UC5347	cdd3 protein - Clo
941	64	5.4	941	2	T12451	hypothetical prote
942	64	5.4	942	2	H69768	conserved hypothet
943	64	5.4	943	2	F89632	protein P13E6.3 [i
944	64	5.4	944	2	T50567	probable ABC-type
945	64	5.4	945	2	C70040	plant-metabolite d
946	64	5.4	946	2	S48358	probable membrane
947	64	5.4	947	2	C95932	probable sugar upt
948	64	5.4	948	2	D83009	probable permease
949	64	5.4	949	2	B83883	sugar transport sy
950	64	5.4	950	2	S36955	cytochrome-c oxida
951	64	5.4	951	2	T29675	hypothetical prote
952	64	5.4	952	2	A48258	dopamine receptor
953	64	5.4	953	2	T11248	NMDH2 dehydrogenas
954	64	5.4	954	2	S56716	protein kinase SPK
955	64	5.4	955	2	G01430	P16 protein - huma
956	64	5.4	956	2	T20271	hypothetical prote
957	64	5.4	957	2	H90587	hypothetical prote
958	64	5.4	958	2	S26031	ubiquitinol-cytochro
959	64	5.4	959	2	G82656	twilching motility
960	64	5.4	960	2	CB4181	probable cytochrom
961	64	5.4	961	1	CBO	ubiquitinol-cytochro
962	64	5.4	962	1	S17419	ubiquitinol-cytochro
963	64	5.4	963	1	S26163	ubiquitinol-cytochro
964	64	5.4	964	1	S43263	ubiquitinol-cytochro
965	64	5.4	965	2	T11414	ubiquitinol-cytochro
966	64	5.4	966	2	S58452	ubiquitinol-cytochro
967	64	5.4	967	2	S58459	ubiquitinol-cytochro
968	64	5.4	968	2	S55594	G protein-coupled
969	64	5.4	969	2	G64667	NA+/H+ antiporter
970	64	5.4	970	2	H71848	probable na+/h+ an
971	64	5.4	971	2	S74522	hypothetical prote
972	64	5.4	972	2	AD1417	drug-efflux transp
973	64	5.4	973	2	A97559	hypothetical prote
974	64	5.4	974	2	AE2779	acyltansferase [i
975	64	5.4	975	2	S26021	NMDH2 dehydrogenas
976	64	5.4	976	2	A55610	corticotropin-rele
977	64	5.4	977	2	H81659	branched-chain ami
978	64	5.4	978	2	E84338	isocitrate dehydro

979	64	5.4	430	1	S32570	malC protein - Str	1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
980	64	5.4	450	2	B40392	alpha-2-adrenergic	1053	63.5	5.3	328	2	D98215	oligopeptide ABC c
981	64	5.4	451	2	A36908	spore cortex penic	1054	63.5	5.3	328	2	T39824	septrin homolog - f
982	64	5.4	455	2	T31258	aromatic oxygenase	1055	63.5	5.3	334	2	B72393	oligopeptide ABC c
983	64	5.4	457	2	AF2975	aminotransferase,	1056	63.5	5.3	334	2	T41037	hypothetical prote
984	64	5.4	457	2	E98307	probable aminotran	1057	63.5	5.3	334	2	T27081	hypothetical prote
985	64	5.4	463	2	AC0281	probable amino aci	1058	63.5	5.3	342	2	A38908	sp40 protein - Sh
986	64	5.4	469	2	H90322	polysaccharide bio	1059	63.5	5.3	344	2	T34981	probable integral
987	64	5.4	492	2	B58931	NMDH2 dehydrogenas	1060	63.5	5.3	355	2	T15203	hypothetical prote
988	64	5.4	503	2	JC7627	cytochrome P450 3A	1061	63.5	5.3	359	2	D90172	hypothetical prote
989	64	5.4	511	2	T40334	hypothetical prote	1062	63.5	5.3	361	2	AE3071	hypothetical prote
990	64	5.4	527	2	T45122	sodium- and chlori	1063	63.5	5.3	365	2	AB3494	oligopeptide trans
991	64	5.4	536	2	T36109	hypothetical prote	1064	63.5	5.3	372	2	S26667	g protein-coupled
992	64	5.4	544	2	C90406	conserved hypochet	1065	63.5	5.3	377	2	B72275	probable aspartate
993	64	5.4	544	2	T13877	NMDH2 dehydrogenas	1066	63.5	5.3	380	1	CBRT	ubiquinol-cytochro
994	64	5.4	562	2	T52481	cytochrome-c oxida	1067	63.5	5.3	381	2	T11312	ubiquinol-cytochro
995	64	5.4	575	2	G75282	probable glutathio	1068	63.5	5.3	387	2	H88012	protein K1084.2 [i
996	64	5.4	586	1	A34400	ezrin [validated]	1069	63.5	5.3	389	2	G75133	hypothetical prote
997	64	5.4	598	2	T05130	hypothetical prote	1070	63.5	5.3	392	2	H71520	probable htn trans
998	64	5.4	602	2	B69805	hypothetical prote	1071	63.5	5.3	395	2	B81358	transmembrane tran
999	64	5.4	608	2	G02640	conserved hypochet	1072	63.5	5.3	398	2	C71682	ubiquinol-cytochro
1000	64	5.4	608	2	G02640	polycystic kidney	1073	63.5	5.3	398	2	D81397	probable periplasm
1001	64	5.4	609	2	P70512	probable ATPase -	1074	63.5	5.3	399	2	B95080	cell division prot
1002	64	5.4	610	2	S37049	H+-exporting ATPas	1075	63.5	5.3	400	2	AG3016	phosphoglycerate k
1003	64	5.4	614	2	A69845	Na+/H+ antiporter	1076	63.5	5.3	401	2	T46306	hypothetical prote
1004	64	5.4	630	2	T47177	hypothetical prote	1077	63.5	5.3	404	1	LABECA	latent membrane pr
1005	64	5.4	654	2	C86677	DNA ligase (NAD) (	1078	63.5	5.3	406	2	T19887	hypothetical prote
1006	64	5.4	657	2	T52460	hypothetical prote	1079	63.5	5.3	423	2	T04915	CDP-diacylglycerol
1007	64	5.4	661	2	T51779	non-phototropic hy	1080	63.5	5.3	423	2	G85255	CDP-diacylglycerol
1008	64	5.4	674	2	T50347	hypothetical prote	1081	63.5	5.3	426	2	A96268	phosphoglycerate k
1009	64	5.4	696	2	AB1566	hypothetical prote	1082	63.5	5.3	426	2	T33299	hypothetical prote
1010	64	5.4	748	2	T10651	hypothetical prote	1083	63.5	5.3	438	2	A82262	conserved hypochet
1011	64	5.4	802	2	A87754	protein C43B11.11	1084	63.5	5.3	444	2	B85789	hypothetical prote
1012	64	5.4	838	2	H82939	conserved hypochet	1085	63.5	5.3	445	2	T16025	hypothetical prote
1013	64	5.4	860	2	T37768	probable vacuolar	1086	63.5	5.3	447	2	P90940	hypothetical prote
1014	64	5.4	874	2	B86322	FA14.8 protein -	1087	63.5	5.3	447	2	S52437	CDP-diacylglycerol
1015	64	5.4	896	2	AF1409	the two components	1088	63.5	5.3	450	2	B96738	hypothetical prote
1016	64	5.4	991	2	S57385	probable membrane	1089	63.5	5.3	452	2	T21118	hypothetical prote
1017	64	5.4	1024	1	RN208F	DNA-directed RNA p	1090	63.5	5.3	461	2	C97187	sugar transferase
1018	64	5.4	1078	2	T19745	hypothetical prote	1091	63.5	5.3	468	2	T48686	hypothetical prote
1019	64	5.4	1081	2	B81303	probable membrane	1092	63.5	5.3	485	2	H90562	mg2+ transport pro
1020	64	5.4	1227	2	A33638	erythrocyte anion	1093	63.5	5.3	487	2	B95059	hypothetical prote
1021	64	5.4	1385	2	T13415	hypothetical prote	1094	63.5	5.3	491	2	B64939	hypothetical prote
1022	64	5.4	1462	1	DJHDAC	DNA-directed DNA p	1095	63.5	5.3	492	2	B90373	sugar transport re
1023	64	5.4	1695	2	JE0084	voltage-gated sodi	1096	63.5	5.3	494	2	S76516	integral membrane
1024	64	5.4	2496	2	A71616	secreted protein p	1097	63.5	5.3	498	2	T48385	transporter like p
1025	63.5	5.3	111	2	S43115	acidic ribosomal p	1098	63.5	5.3	498	2	T16190	NADH dehydrogenase
1026	63.5	5.3	123	2	G71682	NMDH2 dehydrogenas	1099	63.5	5.3	500	2	AF2325	hypothetical prote
1027	63.5	5.3	147	2	AH0495	probable membrane	1100	63.5	5.3	511	2	G90321	NADH dehydrogenase
1028	63.5	5.3	149	2	H70581	hypothetical prote	1101	63.5	5.3	512	1	A70201	hypothetical prote
1029	63.5	5.3	195	2	E71000	hypothetical prote	1102	63.5	5.3	525	2	A49601	nucloeocapsid prote
1030	63.5	5.3	214	2	C90191	conserved hypochet	1103	63.5	5.3	537	2	G82873	conserved hypochet
1031	63.5	5.3	218	2	B71925	csg island protein	1104	63.5	5.3	540	1	I49454	sterol O-acetyltrans
1032	63.5	5.3	218	2	T29205	hypothetical prote	1105	63.5	5.3	544	2	C96943	uncharacterized me
1033	63.5	5.3	231	2	F85679	probable anti-pre	1106	63.5	5.3	551	2	D71969	L-lactate permease
1034	63.5	5.3	238	2	S75336	hypothetical prote	1107	63.5	5.3	555	2	G96744	probable peptide t
1035	63.5	5.3	241	2	F86691	ABC transporter pe	1108	63.5	5.3	567	2	C75340	probable L-lactate
1036	63.5	5.3	242	1	S74794	hypothetical prote	1109	63.5	5.3	567	2	T17588	hyaluronoglucosam
1037	63.5	5.3	246	2	AD3574	branched-chain ami	1110	63.5	5.3	568	2	T17588	sodium/dicarboxyla
1038	63.5	5.3	259	2	AF0106	probable membrane	1111	63.5	5.3	593	2	I46528	protein ZK697.5 [i
1039	63.5	5.3	275	2	E95161	hypothetical prote	1112	63.5	5.3	594	2	B88956	glucose transport
1040	63.5	5.3	275	2	D98027	hypothetical prote	1113	63.5	5.3	605	2	A36361	probable flagellar
1041	63.5	5.3	275	2	G84320	hypothetical prote	1114	63.5	5.3	605	2	H71562	hypothetical prote
1042	63.5	5.3	276	2	E96951	conserved membrane	1115	63.5	5.3	605	2	T43974	hypothetical prote
1043	63.5	5.3	280	2	T16240	hypothetical prote	1116	63.5	5.3	610	2	T44161	ba-type ubiquinol
1044	63.5	5.3	282	2	AB0346	probable ABC trans	1117	63.5	5.3	668	2	B54759	protein kinase C (
1045	63.5	5.3	282	2	E83086	conserved hypochet	1118	63.5	5.3	671	2	B77237	probable type III
1046	63.5	5.3	291	2	AB2939	hypothetical prote	1119	63.5	5.3	681	2	AF0697	hypothetical prote
1047	63.5	5.3	291	2	E98343	hypothetical prote	1120	63.5	5.3	683	2	A85044	killer toxin KHS p
1048	63.5	5.3	291	2	F75571	hypothetical prote	1121	63.5	5.3	708	2	T20314	hypothetical prote
1049	63.5	5.3	313	2	D26596	NMDH2 dehydrogenas	1122	63.5	5.3	741	2	T48189	probable transport
1050	63.5	5.3	315	2	E69365	hypothetical prote	1123	63.5	5.3	760	2	T48189	cell division prot
1051	63.5	5.3	316	2	H86665	ferrichrome ABC tr	1124	63.5	5.3	787	2	A70132	

1125	63.5	5.3	819	2	T19351	1198	63	5.3	480	2	B70367	hypothetical prote
1126	63.5	5.3	841	2	T38703	1199	63	5.3	481	2	S60260	stromatin-like prot
1127	63.5	5.3	843	2	T32487	1200	63	5.3	480	2	C71541	probable na-depend
1128	63.5	5.3	843	2	T41237	1201	63	5.3	491	2	AC1499	transmembrane prot
1129	63.5	5.3	844	2	AD2339	1202	63	5.3	493	2	T02376	hypothetical prote
1130	63.5	5.3	951	2	T08987	1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1131	63.5	5.3	966	2	H97717	1204	63	5.3	508	2	E90594	amino acid permeas
1132	63.5	5.3	1004	2	G87323	1205	63	5.3	509	1	A48528	membrane glycoprot
1133	63.5	5.3	1009	2	S38100	1206	63	5.3	527	2	T40744	probable nuclear d
1134	63.5	5.3	1229	2	S42381	1207	63	5.3	531	2	AH1491	hypothetical prote
1135	63.5	5.3	1351	2	C71607	1208	63	5.3	533	2	T06153	hypothetical prote
1136	63.5	5.3	1388	2	T117269	1209	63	5.3	534	2	A99316	hypothetical prote
1137	63.5	5.3	1407	1	T00558	1210	63	5.3	535	2	AF1835	hypothetical prote
1138	63.5	5.3	1408	2	T47671	1211	63	5.3	562	2	B70081	hypothetical prote
1139	63.5	5.3	1545	2	T42751	1212	63	5.3	565	2	B86359	protein similar to
1140	63.5	5.3	1545	2	T46645	1213	63	5.3	569	2	C70136	flagellar basal-bo
1141	63.5	5.3	1769	2	S53378	1214	63	5.3	574	2	T47566	hypothetical prote
1142	63.5	5.3	2357	2	A59249	1215	63	5.3	579	2	AB2177	hypothetical prote
1143	63.5	5.3	4725	1	A44357	1216	63	5.3	583	2	G84829	probable PIR2 faml
1144	63	5.3	96	1	MMVZB3	1217	63	5.3	584	2	G89789	two-component sens
1145	63	5.3	103	2	T20878	1218	63	5.3	598	2	S66954	probable membrane
1146	63	5.3	175	2	D70945	1219	63	5.3	600	2	B83875	two-component sens
1147	63	5.3	230	2	B81705	1220	63	5.3	608	2	AD2000	ABC transporter At
1148	63	5.3	230	2	T17506	1221	63	5.3	677	2	T26574	hypothetical prote
1149	63	5.3	236	2	F83520	1222	63	5.3	677	2	F95910	probable membrane-
1150	63	5.3	249	2	T01891	1223	63	5.3	682	1	H64485	replicaton licens
1151	63	5.3	257	2	S01165	1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1152	63	5.3	257	2	H65188	1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1153	63	5.3	258	2	F86071	1226	63	5.3	704	2	T13665	NADH2 dehydrogenas
1154	63	5.3	258	2	H91224	1227	63	5.3	712	2	D87418	proton pump, proba
1155	63	5.3	280	2	D84015	1228	63	5.3	729	2	T06127	probable sugar tra
1156	63	5.3	288	2	S36954	1229	63	5.3	737	2	T39547	S-protein secretio
1157	63	5.3	290	2	S48301	1230	63	5.3	738	2	S58612	NADH2 dehydrogenas
1158	63	5.3	301	2	T50001	1231	63	5.3	769	2	G95270	hypothetical prote
1159	63	5.3	306	2	H83620	1232	63	5.3	813	2	T02672	hypothetical prote
1160	63	5.3	313	2	A86743	1233	63	5.3	849	2	C87740	protein H26D21.2 [
1161	63	5.3	322	2	B90013	1234	63	5.3	869	2	S49844	probable membrane
1162	63	5.3	329	2	B87790	1235	63	5.3	943	2	B45082	neurotrophic recep
1163	63	5.3	332	2	B84943	1236	63	5.3	960	2	T17297	hypothetical prote
1164	63	5.3	339	2	D89880	1237	63	5.3	1030	2	A42497	anion exchanger 3,
1165	63	5.3	345	2	T12364	1238	63	5.3	1034	2	H86680	SMI/SNF Family hel
1166	63	5.3	358	2	B83808	1239	63	5.3	1082	2	H70360	cation efflux syst
1167	63	5.3	359	2	S56720	1240	63	5.3	1217	2	B82809	exodeoxyribonuclea
1168	63	5.3	361	2	A45211	1241	63	5.3	1232	2	B34911	band 3-related pro
1169	63	5.3	362	2	T29552	1242	63	5.3	1532	2	JH8438	hypothetical prote
1170	63	5.3	362	2	C69804	1243	63	5.3	1646	2	JH0422	voltage-dependent
1171	63	5.3	364	2	S65009	1244	63	5.3	1854	2	T39035	putative sodium ch
1172	63	5.3	365	2	A42414	1245	63	5.3	2203	2	T42742	voltage-dependent
1173	63	5.3	378	1	S17412	1246	63	5.3	2295	2	B71621	probable membrane
1174	63	5.3	379	1	S17411	1247	63	5.3	4488	1	PR1HM2	genome polypeptin
1175	63	5.3	379	1	S41833	1248	62.5	5.2	107	2	B69262	hypothetical prote
1176	63	5.3	379	1	S41847	1249	62.5	5.2	140	2	B86739	potassium channel
1177	63	5.3	379	1	S43265	1250	62.5	5.2	149	2	B83851	hypothetical prote
1178	63	5.3	379	1	T11492	1251	62.5	5.2	168	2	JC1169	DNA-damage-inducib
1179	63	5.3	379	2	S58085	1252	62.5	5.2	173	2	S67379	hypothetical prote
1180	63	5.3	379	2	S58464	1253	62.5	5.2	178	2	S67379	hypothetical prote
1181	63	5.3	382	2	S47882	1254	62.5	5.2	181	2	G82311	hypothetical prote
1182	63	5.3	386	2	S60646	1255	62.5	5.2	200	2	A71895	hypothetical prote
1183	63	5.3	389	2	H95003	1256	62.5	5.2	232	2	T22698	hypothetical prote
1184	63	5.3	389	2	C97876	1257	62.5	5.2	236	2	F83705	hypothetical prote
1185	63	5.3	391	2	D64541	1258	62.5	5.2	240	2	H70091	hypothetical prote
1186	63	5.3	396	2	E97947	1259	62.5	5.2	244	2	T20810	hypothetical prote
1187	63	5.3	398	2	E70415	1260	62.5	5.2	245	2	S10658	hypothetical prote
1188	63	5.3	405	2	T20902	1261	62.5	5.2	258	2	E91201	type III secretion
1189	63	5.3	411	2	G90154	1262	62.5	5.2	258	2	A86048	esct (imported) -
1190	63	5.3	415	2	S39535	1263	62.5	5.2	274	2	AC2946	hypothetical prote
1191	63	5.3	420	2	A57742	1264	62.5	5.2	274	2	G98336	sorbitol/mannitol
1192	63	5.3	431	2	T23809	1265	62.5	5.2	276	2	G72292	glycerol-3-phospha
1193	63	5.3	448	2	T30982	1266	62.5	5.2	276	2	H83568	probable permease
1194	63	5.3	450	2	A34169	1267	62.5	5.2	280	2	T24579	hypothetical prote
1195	63	5.3	469	2	A82188	1268	62.5	5.2	283	2	T11063	NADH2 dehydrogenas
1196	63	5.3	475	2	S52893	1269	62.5	5.2	289	2	D82504	phosphate ABC tran
1197	63	5.3	478	2	CS9095	1270	62.5	5.2	293	2	AH0075	probable permease

1271	62.5	5.2	296	2	H83460	cytochrome o ubiqu	1344	62.5	5.2	704	2	S46000	probable membrane
1272	62.5	5.2	298	2	T37251	homeobox protein c	1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1273	62.5	5.2	299	2	T26365	hypothetical prote	1346	62.5	5.2	738	2	T27937	hypothetical prote
1274	62.5	5.2	326	2	G90272	hypothetical prote	1347	62.5	5.2	807	2	T28379	ORF MSVII.9 probab
1275	62.5	5.2	333	2	AB1925	hypothetical prote	1348	62.5	5.2	815	2	G97266	mannose-1-phosphat
1276	62.5	5.2	333	2	B89010	hypothetical prote	1349	62.5	5.2	837	2	D71027	hypothetical prote
1277	62.5	5.2	335	2	T41426	hypothetical wtH	1350	62.5	5.2	848	2	A33810	band 3 anion trans
1278	62.5	5.2	349	2	H95060	ABC transporter, p	1351	62.5	5.2	865	2	AB1658	probable membrane
1279	62.5	5.2	349	2	D97929	hypothetical prote	1352	62.5	5.2	881	2	G96574	hypothetical prote
1280	62.5	5.2	352	2	B81450	probable integral	1353	62.5	5.2	971	2	H71719	hypothetical prote
1281	62.5	5.2	365	2	R83829	hypothetical prote	1354	62.5	5.2	1082	2	T41988	hypothetical prote
1282	62.5	5.2	365	2	B82210	amino acid ABC tra	1355	62.5	5.2	1144	2	AB1983	probable DNA-dirc
1283	62.5	5.2	369	2	C88030	protein F46P5.10 f	1356	62.5	5.2	1195	2	C87691	hypothetical prote
1284	62.5	5.2	370	2	C69309	conserved hypotet	1357	62.5	5.2	1291	2	T17242	hypothetical prote
1285	62.5	5.2	379	1	S17407	ubiquinol-cytochro	1358	62.5	5.2	1391	2	T20642	hypothetical prote
1286	62.5	5.2	379	2	S58462	ubiquinol-cytochro	1359	62.5	5.2	1397	2	B87998	protein F09C3.1 f1
1287	62.5	5.2	379	2	S58057	ubiquinol-cytochro	1360	62.5	5.2	1576	2	T21172	hypothetical prote
1288	62.5	5.2	382	2	A72373	conserved hypotet	1361	62.5	5.2	1676	2	E71410	probable centromer
1289	62.5	5.2	383	1	A44227	omega-3 fatty acid	1362	62.5	5.2	1687	2	T43144	vitellogenin II pr
1290	62.5	5.2	383	2	F84771	hypothetical prote	1363	62.5	5.2	1951	2	B43963	RNA viral polymera
1291	62.5	5.2	383	2	T31738	hypothetical prote	1364	62.5	5.2	2150	2	S13553	hypothetical prote
1292	62.5	5.2	388	2	C64722	Na+/H+-exchanging	1365	62.5	5.2	112	2	T11073	hypothetical prote
1293	62.5	5.2	391	2	A86632	aromatic amino aci	1366	62.5	5.2	132	2	D82954	probable centromer
1294	62.5	5.2	399	2	H84087	hypothetical prote	1367	62.5	5.2	174	2	B84028	cell-shape determi
1295	62.5	5.2	404	2	H83249	bodium/glutamate s	1368	62.5	5.2	175	1	IMECB	collicin B immunity
1296	62.5	5.2	405	1	Q08B35	BRF3 protein - hu	1369	62.5	5.2	198	2	B97217	uncharacterized co
1297	62.5	5.2	406	2	H89006	protein T22F3.11 f	1370	62.5	5.2	201	2	G90134	hypothetical prote
1298	62.5	5.2	409	2	C89942	conserved hypotet	1371	62.5	5.2	206	2	F89840	conserved hypotet
1299	62.5	5.2	413	2	AC1369	multidrug resistanc	1372	62.5	5.2	209	2	A88656	protein F37C4.1 f1
1300	62.5	5.2	417	2	T51457	glucose 6 phosphat	1373	62.5	5.2	209	2	T32573	hypothetical prote
1301	62.5	5.2	420	2	D95018	conserved hypotet	1374	62.5	5.2	225	2	B65127	type 4 prepillin-11
1302	62.5	5.2	420	2	B97891	conserved hypotet	1375	62.5	5.2	242	1	F75433	probable phosphos
1303	62.5	5.2	422	2	C70518	flagellin importe	1376	62.5	5.2	247	2	AC1332	potassium channel
1304	62.5	5.2	425	2	B97172	flagellin (importe	1377	62.5	5.2	273	2	E70010	dihydrolipoamide S
1305	62.5	5.2	426	2	A72080	CT266 hypothetical	1378	62.5	5.2	285	2	H95943	probable sugar upt
1306	62.5	5.2	426	2	B86542	hypothetical prote	1379	62.5	5.2	287	2	A69838	transcription regu
1307	62.5	5.2	431	2	H84069	hypothetical prote	1380	62.5	5.2	288	2	G36953	cytochrome-c oxida
1308	62.5	5.2	440	2	T20092	hypothetical prote	1381	62.5	5.2	288	2	C83356	probable permease
1309	62.5	5.2	442	1	J01042	endothelin recepto	1382	62.5	5.2	298	2	T29189	hypothetical prote
1310	62.5	5.2	443	2	F30010	NMDH2 dehydrogenas	1383	62.5	5.2	305	2	T43972	hypothetical prote
1311	62.5	5.2	443	2	T08136	probable omega-6 d	1384	62.5	5.2	306	2	A10209	probable sugar ABC
1312	62.5	5.2	452	2	G85647	hypothetical prote	1385	62.5	5.2	306	2	T41290	conserved hypotet
1313	62.5	5.2	452	2	G90787	hypothetical prote	1386	62.5	5.2	312	2	S48851	chalcone reductase
1314	62.5	5.2	452	2	G64844	probable membrane	1387	62.5	5.2	312	2	S48849	hypothetical prote
1315	62.5	5.2	455	2	D97217	glycosyltransferas	1388	62.5	5.2	315	2	T24621	hypothetical prote
1316	62.5	5.2	457	2	F69662	UDP-N-acetylmuramo	1389	62.5	5.2	331	2	AB3117	hypothetical prote
1317	62.5	5.2	459	2	AP3284	high-affinity bran	1390	62.5	5.2	344	2	T05987	hypothetical prote
1318	62.5	5.2	461	2	S57713	probable mannosiyl	1391	62.5	5.2	345	2	T32203	hypothetical prote
1319	62.5	5.2	468	2	A49131	inositol 1,4,5-tri	1392	62.5	5.2	351	2	C86408	F3H9.12 protein -
1320	62.5	5.2	470	2	C70641	hypothetical prote	1393	62.5	5.2	352	2	C98170	hypothetical prote
1321	62.5	5.2	487	2	S73161	hypothetical prote	1394	62.5	5.2	353	2	T42971	hypothetical prote
1322	62.5	5.2	490	2	T40116	hypothetical prote	1395	62.5	5.2	360	2	A53611	interleukin-8 rece
1323	62.5	5.2	492	2	AC0768	probable transmemb	1396	62.5	5.2	360	2	T33260	hypothetical prote
1324	62.5	5.2	494	1	T15502	hypothetical prote	1397	62.5	5.2	362	2	B57641	G protein-coupled
1325	62.5	5.2	501	2	JN0539	head protein sps -	1398	62.5	5.2	363	2	S42379	hypothetical prote
1326	62.5	5.2	502	2	C86263	hypothetical prote	1399	62.5	5.2	370	2	H84111	response regulator
1327	62.5	5.2	505	2	S44647	f42h10.1 protein -	1400	62.5	5.2	377	2	T05427	hypothetical prote
1328	62.5	5.2	507	2	S52677	probable membrane	1401	62.5	5.2	379	2	S58457	ubiquinol-cytochro
1329	62.5	5.2	546	2	AB0571	probable membrane	1402	62.5	5.2	379	2	E58851	ubiquinol-cytochro
1330	62.5	5.2	547	2	S64332	probable membrane	1403	62.5	5.2	381	2	T11440	probable two-compo
1331	62.5	5.2	568	2	S64567	probable membrane	1404	62.5	5.2	383	2	C95965	bicyclomyacin resis
1332	62.5	5.2	569	2	T22928	hypothetical prote	1405	62.5	5.2	398	1	B64112	hypothetical prote
1333	62.5	5.2	572	2	T11478	NMDH2 dehydrogenas	1406	62.5	5.2	399	2	F72417	translocation prot
1334	62.5	5.2	578	2	I56215	interleukin-10 rec	1407	62.5	5.2	400	2	JC5279	cell-division prot
1335	62.5	5.2	580	2	T02596	hypothetical prote	1408	62.5	5.2	409	2	AB1565	xylose operon regu
1336	62.5	5.2	608	2	T11451	NMDH2 dehydrogenas	1409	62.5	5.2	402	2	D70186	conserved hypotet
1337	62.5	5.2	608	2	T34381	hypothetical prote	1410	62.5	5.2	403	2	B69338	cbs domain protein
1338	62.5	5.2	610	2	A28798	myosin-light-chain	1411	62.5	5.2	411	2	H72084	protein-tyrosine-p
1339	62.5	5.2	621	2	B95897	probable cellulose	1412	62.5	5.2	432	1	A34845	hypothetical prote
1340	62.5	5.2	638	2	G02068	white homology - hu	1413	62.5	5.2	432	2	T21880	hypothetical prote
1341	62.5	5.2	668	2	T18688	hypothetical prote	1414	62.5	5.2	444	2	T47737	probable transmemb
1342	62.5	5.2	695	2	T04073	intensifier 1 prot	1415	62.5	5.2	444	2	B81367	hypothetical prote
1343	62.5	5.2	697	2	T19254	hypothetical prote	1416	62.5	5.2	454	2	H65054	hypothetical prote

1417	62	5.2	458	2	A84487	probable replicati
1418	62	5.2	466	2	AH1800	transmembrane effl
1419	62	5.2	474	2	E64232	hypothetical prote
1420	62	5.2	483	2	S46124	nuclear protein EN
1421	62	5.2	487	2	T05271	probable 3-oxoacyl
1422	62	5.2	497	1	S53834	NMDH2 dehydrogenas
1423	62	5.2	497	2	S66843	probable membrane
1424	62	5.2	499	2	B81914	probable periplasm
1425	62	5.2	502	2	AE2372	hypothetical prote
1426	62	5.2	514	2	A96671	Ammonium transport
1427	62	5.2	528	1	ACCH2N	nicotinic acetylch
1428	62	5.2	555	2	T08869	protein P2 - Acyryl
1429	62	5.2	567	2	S29498	lymphocyte antigen
1430	62	5.2	582	2	S19424	hypothetical prote
1431	62	5.2	585	2	T02360	hypothetical prote
1432	62	5.2	600	2	AD3138	hypothetical prote
1433	62	5.2	600	2	H98149	ATP-binding transp
1434	62	5.2	630	2	H83686	PTS system, beta-g
1435	62	5.2	644	2	T20034	hypothetical prote
1436	62	5.2	660	2	A44432	amino acid transpo
1437	62	5.2	667	2	T20739	hypothetical prote
1438	62	5.2	675	1	S46952	phosphotransferase
1439	62	5.2	675	2	T20822	hypothetical prote
1440	62	5.2	678	2	F71921	hypothetical prote
1441	62	5.2	702	2	T03903	hypothetical prote
1442	62	5.2	707	2	A35804	nucleolin - human
1443	62	5.2	724	1	HBM884	heat shock protein
1444	62	5.2	739	2	T25030	hypothetical prote
1445	62	5.2	743	2	A29232	101k malaria antiq
1446	62	5.2	750	2	S73829	protein ABC trans
1447	62	5.2	756	2	A88679	protein H06H21.10
1448	62	5.2	791	2	A46616	cytochrome-c oxida
1449	62	5.2	810	1	A33380	interleukin-4 rece
1450	62	5.2	841	2	T09455	vacuolar assembly
1451	62	5.2	848	2	E95092	antipeptidase N (
1452	62	5.2	864	2	T42556	tegument protein 1
1453	62	5.2	872	1	TNBEH	97K alpha trans-in
1454	62	5.2	911	2	S70958	ocna protein - Vib
1455	62	5.2	932	2	C70131	penicillin-binding
1456	62	5.2	950	1	FWBYR1	Ca2+-transporting
1457	62	5.2	1002	2	G97217	conserved membrane
1458	62	5.2	1024	2	AE3557	acridflavin resista
1459	62	5.2	1030	2	T13163	Rab6 GTPase activa
1460	62	5.2	1031	2	T43458	hypothetical prote
1461	62	5.2	1041	2	T29010	hypothetical prote
1462	62	5.2	1242	2	G88480	protein C16A3.7 [1
1463	62	5.2	1273	2	G96767	unknown protein P2
1464	62	5.2	1283	2	T18939	hypothetical prote
1465	62	5.2	1321	2	A60165	sodium channel pro
1466	62	5.2	1780	2	T20695	hypothetical prote
1467	62	5.2	1802	2	T33783	hypothetical prote
1468	62	5.2	6359	2	T31679	baclitracin synthe
1469	61.5	5.1	99	2	B99233	hypothetical prote
1470	61.5	5.1	134	2	B99233	hypothetical prote
1471	61.5	5.1	149	2	C86655	hypothetical prote
1472	61.5	5.1	150	2	S43955	probable NMDH2 deh
1473	61.5	5.1	150	2	S77185	hypothetical prote
1474	61.5	5.1	162	2	AF2618	lipoprotein signal
1475	61.5	5.1	162	2	E97400	hypothetical prote
1476	61.5	5.1	163	2	JC5045	epithelial membran
1477	61.5	5.1	173	2	H97775	hypothetical prote
1478	61.5	5.1	176	2	G89947	hypothetical prote
1479	61.5	5.1	176	2	S40726	hypothetical prote
1480	61.5	5.1	183	2	H70478	hypothetical prote
1481	61.5	5.1	185	2	H69317	conserved hypochet
1482	61.5	5.1	190	2	A26630	conserved hypochet
1483	61.5	5.1	212	2	A83511	conserved hypochet
1484	61.5	5.1	225	2	T19811	hypothetical prote
1485	61.5	5.1	264	2	T18998	hypothetical prote
1486	61.5	5.1	272	2	G82888	hypothetical prote
1487	61.5	5.1	272	2	T28980	hypothetical prote
1488	61.5	5.1	274	2	S42168	NMDH2 dehydrogenas
1489	61.5	5.1	276	2	F72342	conserved hypochet

1490	61.5	5.1	278	2	D83080	hypothetical prote
1491	61.5	5.1	279	2	AG0421	sugar transport sy
1492	61.5	5.1	284	2	AC3429	peroxamine synthet
1493	61.5	5.1	289	2	F91269	hypothetical prote
1494	61.5	5.1	289	2	D86110	hypothetical prote
1495	61.5	5.1	290	2	AE0947	ribonuclease BN (E
1496	61.5	5.1	292	2	AE1539	sugar ABC transport
1497	61.5	5.1	293	2	C90032	hypothetical prote
1498	61.5	5.1	293	2	A83710	ABC transporter (p
1499	61.5	5.1	293	2	B69866	transcription regu
1500	61.5	5.1	294	2	AD0886	probable oxidoredu

## ALIGNMENTS

RESULT 1  
 138027  
 MLN 64 protein - human  
 C/Species: Homo sapiens (man)  
 C/Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C/Accession: I38027; S60682  
 R/Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Uidreau, R.,  
 Genomics 28, 367-376, 1995  
 A/Title: Identification of four novel human genes amplified and overexpressed in breast c  
 A/Reference number: I37080; MUID:96039245; PMID:7490069  
 A/Accession: I38027  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-445 <RES>  
 A/Cross-references: UNIPROT:Q14849; EMBL:X80196; NID:G951278; PIDN:CAA56489.1; PID:G95127;  
 A/Note: submitted to the EMBL Data Library, July 1994  
 C/Genetics:  
 A/Gene: MLN64

Query Match 55.6%; Score 664; DB 2; Length 445;  
 Best Local Similarity 56.2%; Pred. No. 1.2e-54;  
 Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

QY	1	MNHP----	EDMENL-----	TGSSQSHASLRNHSINPQLMARISYGREKKISDV	51
DB	1	MSKLPBELTRDLRSIPAVASLSGSSLSHSSQSLHPPE-----	-----	-----	49

QY	52	RRFFCLFVFEDLLFVTLMTIIEINVGIEENTLEKVMQDYSSYPDIFLAVERKVL	111
DB	50	RRFFCLFVFYDILLFISLMTIIEINVTGIRKNLEQETIQNFKTSFDDIVLAFRRSGL	109

QY	112	ILAVAVCRRLHMMVAALITVAVTSAPFLAKVILSKLSQGAFGVLPPIISFLAMIEITWFL	171
DB	110	ILGAVAVQLRHMVAVITTVSSAFILVKYILSELISKGAFGVLPVIVSVLMLETWFL	169

QY	172	DFKVLPGAEERRLILVQDASRAAII-EGSLSDGQFYSPPSSEAGSE-EAEEKQDSEK	229
DB	170	DFKVLPGAEERHMYLAQVAVARGPILFSGALSCGFYSPPSFAGSDNESDEEVGKK	229

RESULT 2  
 T16170  
 hypothetical protein F26F4.4 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: T16170  
 R/Fulton, U.  
 submitted to the EMBL Data Library, March 1996  
 A/Description: The sequence of C. elegans cosmid F26F4.  
 A/Reference number: Z18471  
 A/Accession: T16170  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-478 <FUL>  
 A/Cross-references: UNIPROT:Q19819; EMBL:U12964; NID:G1213452; PID:G529202; PIDN:AAA9121;  
 A/Experimental source: strain Bristol N2  
 C/Genetics:



A:Gene: CESP.F26P4.4  
A:Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1  
Query Match 17.1%; Score 204; DB 2; Length 478;  
Best Local Similarity 26.5%; Pred. No. 2.7e-11;  
Matches 56; Conservative 36; Mismatches 73; Indels 46; Gaps 6;  
Qy 42 GREKGGSDVRRFTCLFVTFDLLFVTLMLIT-----ELNVNGIENTLEK 86  
Db 69 GSGRIGVSKRKRIIVTFPDTSTIILMLCTVTRDDMDKVFENEINT-----FNP 121  
Qy 87 EVMQDYSSYFDIFLLAVFRFKVLIAVAVCRLRHMAIALTTAVTSAPFLAVILSKL 146  
Db 122 KFLIRI-----SLFDIVLLAVRMLILGVYGCIVKQWTVVAFTTLASSAYILMKVLFYFN 177  
Qy 147 FSGCAFQVLPIL--SFLIWMETWFLDPKVLPOEAEEENLLIVQDASERAAALPGSLD 205  
Db 178 HSSAVPPLLLITLTSFTLWSEFLMPQILPRERYARREL-----DGIEN 224  
Qy 206 GQFYSPPESA-----GSEAEKQDESKP 230  
Db 225 PEFETDEARSNNRRGRQONGSGNSEAP 255

## RESULT 3

hypothetical protein dppB-1 (imported) - Sulfolobus solfataricus  
A:Accession: H90281  
C:Species: Sulfolobus solfataricus  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C/Accession: H90281  
R:Sheng, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayes, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.  
arrest, R.A.; Ragan, M.A.; Senen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: H90281  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-348 <KIR>  
A:Cross-references: UNIPROT:Q9Y700; GB:AE006641; NID:g13814471; PIDN:AAK41511.1; GSPDB:C  
A:Genetics:  
A:Gene: dppB-1  
Query Match 8.6%; Score 102.5; DB 2; Length 348;  
Best Local Similarity 23.7%; Pred. No. 0.066;  
Matches 49; Conservative 35; Mismatches 66; Indels 57; Gaps 9;  
Qy 15 SQSSHASLRNHSINPTQLMARISYEGREKKGISDVRRFTCLFVTFDLLFVTLMLIEL 74  
Db 46 AQFSQTLFKNAHNLNSTQIQLAVEKY--RE-----SLIAAYGL 81  
Qy 75 NVNNGIENTLEK-----EVMQDYSSYFDIFLLAVFRFKVLIAVAVCRLRHMAIAL 128  
Db 82 N-----OPTIDKVFQIMNLMRFDFGAYF--LQAPSSGREVSSILIAVLPN-----TTL 130  
Qy 129 TTAVTSAFLKAVILSKLFGSGAF--GYVLPIISFLIWMETWFLDPKVLPOEAEEENLL 187  
Db 131 FTTATIVFIYAGTIIGLSKSKMEKVIATIAIVHSIPTWLGK-----VL 178  
Qy 188 IVQDASERAAALPGSLDQGFYSPES 214  
Db 179 IAAALAVAVKVPFGWMTS---VPPPKN 202  
RESULT 4  
D75080  
glucose-1-phosphate thymidyltransferase related protein PAB2433 - Pyrococcus abyssi (S  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: D75080  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc  
A:Reference number: A75001  
A:Accession: D75080  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-424 <KAW>  
A:Cross-references: UNIPROT:Q9UZM1; GB:AJ248286; GB:AL096836; NID:95458366; PIDN:CAB4994;  
A:Experimental source: strain Orsay  
C:Genetics:  
C:Gene: PAB2433  
C:Superfamily: Aquifex aeolicus glucose-1-phosphate thymidyltransferase

Query Match 7.8%; Score 93.5; DB 2; Length 424;  
Best Local Similarity 21.9%; Pred. No. 0.59;  
Matches 47; Conservative 25; Mismatches 72; Indels 71; Gaps 7;

Qy 5 PEDMEN-----LNGSSHASLRNHSINPTQLMARISYEGRE 44  
Db 207 PEDIKKARKLIIVTSYKVGDFISRLNRKISTRSLALVEHVTPQM----- 255  
Qy 45 KKGISDVRRFTCLFVTFDL--LFTLLMIIEIANVG-----GIENLEKVMQDY 93  
Db 256 -----TIVTFLEGISALNPFISVPIAGILYQVSSILDGVDGSIARARQTSK 303  
Qy 94 YSSYFDIFLLAVFRFK-VILIAVAVCRLRHMAIALTTAVTSAPL-----L 138  
Db 304 FGCVFSDILDRYVDFELLILAVYSIREPLMAIALMPSAMVSYSYTERFKGAYCVA 363  
Qy 139 AKYI--LSKLFSGAFQVLPPIISFLIWMETWFL 171  
Db 364 YKVIPLARKVPGKRDERIFLTMLLTWGMIKALFL 398

## RESULT 5

T43048  
calcium channel alpha-1 chain - Cyanea capillata  
C:Species: Cyanea capillata  
C>Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C/Accession: T43048  
R:Jezioriski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.  
A:Title: Cloning and functional expression of a voltage-gated calcium channel subu  
A:Reference number: Z22300; WUID:98380510; PMID:9712913  
A:Accession: T43048  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1911 <JEZ>  
A:Cross-references: UNIPROT:O02038; EMBL:U03075; NID:g1947095; PID:g1947096; PIDN:AA630;  
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
C:Keywords: transmembrane protein

Query Match 7.5%; Score 90; DB 2; Length 1911;  
Best Local Similarity 23.5%; Pred. No. 7.3;  
Matches 43; Conservative 33; Mismatches 59; Indels 48; Gaps 9;

Qy 5 PEDMENALTGSSHASLRNHSINPTQLM-----ARISYEGREKKGISDV----- 51  
Db 791 PEDVE--LGNPKSKNGTLRMGETSTSEMSBGEARIRPRLSELMLKQIDPMPPESS 848  
Qy 52 -----RRTCLFVTPELLFVT--LMIIEIANVGIENTLEKVMQDYSSYFDI 100  
Db 849 FFIISANNKRLRYCYRLAVNKKIFINSILVILIMSSVALAEDPIGRDVA--NKILGFDI 907  
Qy 101 FLIAVFRFKVL--LAVAV-----CR-----LRHMAIALTT--AVTSAPFLA 139  
Db 908 FTTAMFTFEVTVKMAIFGVILHRSFCRSPFNQDLVIYAVSMAALMLSGSATSVRIL 967  
Qy 140 KVI 142  
Db 968 RVL 970

## RESULT 6



Matches	38;	Conservative	35;	Mismatches	50;	Indels	75;	Gaps	8;
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A/Cross-references: UNIPROT:Q34192; EMBL:X56015; NID:g12879; PIDN:CAA39492.1; PID:g12882  
C/Genetics:

A/Cross-references: UNIPROT:Q34192; EMBL:X56015; NID:g12879; PIDN:CAA39492.1; PID:g12882  
C/Genetics:

A:Gene: ND5  
A:Genome: mitochondrion  
A:Genetic code: SGC6  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 83; DB 1; Length 590;

Best Local Similarity 23.9%; Pred. No. 8.4; Mismatches 37; Indels 42; Gaps 7;

Matches 32; Conservative 23; Mismatches 37; Indels 42; Gaps 7;

QY 55 FCLFVTP-----DL-----FTLLMIIELVNGIGIENTLEKEVQDYSSYFDIFLLAVF 106

DB 95 FILFVAFYVYVYDLMKRFNIFWVFLCNVFI-----LSYDYLTAFCGWEILGLF 146

QY 107 RPKVLLIYAVCRHRHMAALTTAVTSAPLAKVILSKLPSQAGFVYPIISFLAWI 166

DB 147 SF--PLISY-----FWYREFALKFSPKSPFISKI-----GDVLLLSFVWTFI 187

QY 167 ET-----WFLDP 173

DB 188 STGYGMNFYFVNP 201

## RESULT 14

B29835  
Tras protein - Escherichia coli plasmid pED208

C:Species: Escherichia coli  
C:Date: 04-Aug-1988 #sequence\_revision 04-Aug-1988 #text\_change 09-Jul-2004

C:Accession: B29835

R./Finlay, B.B.; Paranchych, W.

J. Bacteriol. 166, 713-721, 1986

A:Title: Nucleotide sequence of the surface exclusion genes tras and trar from the IncF-

A:Reference number: A29835; MUID:86223783; PMID:3011738

A:Accession: B29835

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-186 <FIN>

A:Cross-references: UNIPROT:P14498

A:Genetics:

A:Genome: plasmid

Query Match 6.9%; Score 82.5; DB 2; Length 186;

Best Local Similarity 23.8%; Pred. No. 2.4;

Matches 31; Conservative 24; Mismatches 40; Indels 35; Gaps 6;

QY 61 FDLFVTLMIIELVNGIGIENTLEKEVQDYSSYFDIFLL-----AVFREKVLILAY 115

DB 44 FOLLFI-----IPDIFINSNR-----DYH--YFDTFVITLGSNAFFSLVFLMSTY 87

QY 116 AVCRHRHMAALTTAVTSAPLAKVILSKLPSQAGFVYPIISFLAW 165

DB 88 NLVSLK-----ISLGSRTTEOSVLKLVKINSYGOFLMVVNAIVGCVLLSSGERFVAGL 143

QY 166 IETWFLDPKV 175

DB 144 GPSWFTVYLI 153

## RESULT 15

C64227  
hypothetical protein homolog MG247 - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: C64227

R./Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M.; Furman, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

; C.A.; Venter, J.C.  
Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

A:Reference number: A64200; MUID:96026346; PMID:7569993

A:Accession: C64227

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-239 <TIGR>  
A:Cross-references: UNIPROT:P47489; GB:U39703; GB:I43967; MUID:G3844835; PIDN:AACT1467.1;  
A:Experimental source: strain G-37  
A:Genetics:  
C:Genetic code: SGC3  
C:Superfamily: Escherichia coli ygiH protein

Query Match 6.9%; Score 82.5; DB 1; Length 239;

Best Local Similarity 21.7%; Pred. No. 3.3; Mismatches 54; Indels 39; Gaps 8;

Matches 33; Conservative 26; Mismatches 54; Indels 39; Gaps 8;

QY 42 GREKGISDVRRATF-----CLFVTFDLFVTL--WIELVNGIGIENTLEKEVQDY 92

DB 42 GSKNPATNSMRVFGKIGFLVAIFDAFGFAFLTWIL---FRGLQGYLTKKYQST 98

QY 93 YSSYFDIFLLAV-----FRK---VILLAVNCRHRHMAI-----ALTAVTSA 135

DB 99 YFLSYSCFPAATGHIIFPLIFKFKGKALATGGSILAIISLMWFLICLAIMWITLTKY 158

QY 136 FLAKVILSKLPSQAGFVYPIISFLAWI 167

DB 159 VSLASLITP-----FVLAVI-ILIRWLD 180

Search completed: May 17, 2005, 10:23:07  
Job time : 35 secs

**BEST AVAILABLE COPY**

GenCore version 5.1.6  
 OM protein - protein search, using sw model  
 Run on: May 17, 2005, 10:19:51 ; Search time 75 Seconds  
 (without alignments)  
 1206.692 Million cell updates/sec

Title: US-10-063-518-14  
 Perfect score: 1195  
 Sequence: 1 MNHLPRDMENALTGSSQSHN.....EAGSEAEKQDEKPLLEL 234  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 2105692 seqs, 386760381 residues  
 Total number of hits satisfying chosen parameters: 2105692  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries

Database :  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AAU29056	standard; protein; 234 AA.		
DE	Human PRO polypeptide sequence #33.			
PD	WO200168848-A2.			
PD	20-SEP-2001.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 4; Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;		
RESULT 2				
ID	AAM39929	standard; protein; 234 AA.		
DE	Human polypeptide SEQ ID NO 3074.			
PD	WO200153312-A1.			
PD	26-JUL-2001.			
PA	(HYSE-) HYSEQ INC.			
Query Match	100.0%;	Score 1195; DB 4; Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;		
RESULT 3				
ID	AAB87532	standard; protein; 234 AA.		
DE	Human PRO1864.			
PD	WO200116318-A2.			
PD	08-MAR-2001.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 4; Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;		
RESULT 4				
ID	ABG5857	standard; protein; 234 AA.		
DE	Human secreted/transmembrane protein PRO1864.			
PD	US2002119130-A1.			
PD	29-AUG-2002.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 5; Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;		
RESULT 5				
ID	ABB84847	standard; protein; 234 AA.		
DE	Human PRO1864 protein sequence SEQ ID NO:62.			
PD	WO200200690-A2.			
PD	03-JAN-2002.			
PA	(GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 5; Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;		
RESULT 6				
ID	ABB95453	standard; protein; 234 AA.		

DE	Human angiogenesis related protein PRO1864 SEQ ID NO: 62.
PD	WO200208284-A2.
PD	31-JAN-2002.
PA	(GETH ) GENENTECH INC.
PA	(BAKE/) BAKER K P.
PA	(FERR/) FERRARA N.
PA	(GERB/) GERBER H.
PA	(GERR/) GERRITSEN M E.
PA	(GODD/) GODDARD A.
PA	(GODD/) GODOWSKI P J.
PA	(GURN/) GURNEY A L.
PA	(HILL/) HILLMAN K J.
PA	(MARS/) MARSTERS S A.
PA	(PANJ/) PAN J.
PA	(PAON/) PAONT N F.
PA	(STEP/) STEPHAN J F.
PA	(WATA/) WATANABE C K.
PA	(WILT/) WILTIAMS P M.
PA	(WOOD/) WOOD W I.
Query Match	100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 7	
ID	ABU58432
DE	Human PRO polypeptide #33.
PD	US2003027272-A1.
PD	06-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 8	
ID	ABU87980
DE	Novel human secreted and transmembrane protein PRO1864.
PD	US2003032127-A1.
PD	13-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 9	
ID	ABU84295
DE	Human secreted/transmembrane protein (PRO) #33.
PD	US2003032112-A1.
PD	13-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 10	
ID	ABR66169
DE	Human secreted polypeptide PRO1864, SEQ ID NO:66.
PD	US2003027278-A1.
PD	06-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 11	
ID	ABR65559
DE	Human secreted polypeptide PRO1864, SEQ ID NO:66.
PD	US2003036159-A1.
PD	20-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 12	
ID	ABU99499
DE	Human secreted/transmembrane protein (PRO) #33.
PD	US2003040070-A1.
PD	27-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 13	
ID	ABU82738
DE	Human PRO polypeptide #33.
PD	US2003032113-A1.
PD	13-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 14	
ID	ABU89859
DE	Novel human secreted and transmembrane protein PRO1864.

PN US2003036147-A1.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 15  
ID ABR68108 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 16  
ID AUB96161 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 17  
ID AUB92592 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 18  
ID ABO08669 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 19  
ID ABO02721 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 20  
ID ABR74875 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 21  
ID ABR94637 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 22  
ID AUB85610 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 23  
ID AUB98770 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 24  
ID AUB97985 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003017544-A1.  
PD 23-JAN-2003.

Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 25  
ID AUB91691 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 26  
ID AUB9384 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 27  
ID AUB86225 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 28  
ID AUB67438 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 29  
ID AUB80466 standard; protein; 234 AA.  
DE Human PRO protein #33.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 30  
ID AUB90882 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 31  
ID ABO33941 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein PRO1864.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 32  
ID ABR9384 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 33  
ID ABR98774 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.3e-131;  
RESULT 34  
ID ABO16297 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.



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PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 35
ID ABR92197 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 36
ID ABO1838 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 37
ID ABR78259 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 38
ID ABR3937 standard; protein; 234 AA.
DE Human prostate selective polypeptide Pr340.
PN WO2003014298-A2.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 39
ID ABO1958 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018183-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 40
ID ABO84995 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 41
ID ABO0134 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 42
ID ABO11466 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 43
ID ABO02111 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 44
ID ABO8685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN 16-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 45
ID ABO83380 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 46
ID ABO06181 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 47
ID ABR59217 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 48
ID ABO09279 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 49
ID ABO19143 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036118-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 50
ID ABO11161 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 51
ID ABR66779 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 52
ID ABO15992 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 53
ID ABO13698 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 54
ID ABO71512 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003013855-A1.
PD 16-JAN-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 55
ID ABU65601 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, SEQ ID 66.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 56
ID ABO07449 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 57
ID ABO03636 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 58
ID ABR67084 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 59
ID ABO15687 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 60
ID ABU55968 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, PRO1864.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 61
ID ABU72293 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 62
ID ABU65296 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 63
ID ABU95241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 64
ID ABU71144 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 65
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 66
ID ABR69995 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 67
ID ABR69328 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 68
ID ABO01469 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 69
ID ABU81271 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 70
ID ABR60068 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 71
ID ABR58287 standard; protein; 234 AA.
DE BC0092 protein #SEQ ID 20.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 72
ID ABU90966 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 73
ID ABR67803 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 74
ID ABR65191 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027268-A1.
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PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 75
ID ABR6413 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 76
ID ABR71825 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 77
ID ABR85305 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 78
ID ABR88995 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 79
ID ABR83075 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 80
ID ABR94931 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 81
ID ABR90479 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 82
ID ABR93990 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 83
ID ABR93641 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 84
ID ABR6486 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 85
ID ABR27287 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO1864.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 86
ID ABR68718 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 87
ID ABR06534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 88
ID ABR99079 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 89
ID ABR56963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 90
ID ABR8915 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 91
ID ABR82202 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 92
ID ABR7213 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 93
ID ABR83685 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 94
ID ABR08059 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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RESULT 95  
ID ABU92482 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein PRO1864.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 96  
ID ABU81770 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 97  
ID ABU65934 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 98  
ID ABU81152 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 99  
ID ABR59763 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 100  
ID ABU93951 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 101  
ID ABU99804 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 102  
ID ABR66474 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 103  
ID ABR90692 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 104  
ID ABO5367 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 105  
ID ABU94319 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 106  
ID ABU79201 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 107  
ID ABU86530 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 108  
ID ABU86635 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 109  
ID ABU94624 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 110  
ID ABO04551 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 111  
ID ABR70300 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 112  
ID ABU98465 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 113  
ID ABR65864 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 114  
ID ABR64581 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 115

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ID ABU79506 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 116
ID ABU79506 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 117
ID ABU95856 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 118
ID ABU91076 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 119
ID ABU90169 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 120
ID ABO0584 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 121
ID ABO1085 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 122
ID ABR70910 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 123
ID ABU98269 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 124
ID ABU87518 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003023293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 125
ID ABU91386 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 126
ID ABU9274 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 127
ID ABU84600 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 128
ID ABR63690 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 129
ID ABU80067 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 130
ID ABU82481 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 131
ID ABU93336 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 132
ID ABO09889 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 133
ID ABO08974 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 134
ID ABU96445 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 135
ID ABU10542 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.
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PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 136  
ID ABU72115 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 137  
ID ABU95551 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 138  
ID ABU96760 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 139  
ID ABR70605 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 140  
ID ABO04956 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US200308352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 141  
ID ABO08364 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 142  
ID ABO05571 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 143  
ID ABR73960 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 144  
ID ABR95552 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 145

ID ABR80849 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 146  
ID ABR81154 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 147  
ID ABM00850 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 148  
ID ABR8452 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 149  
ID ABW7273 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 150  
ID ABO28757 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 151  
ID ABO31502 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 152  
ID ABM07919 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 153  
ID ABO40399 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 154  
ID ABO35824 standard; protein; 234 AA.

ID	HUMAN PRO polypeptide #33.
PID	US2003068701-AI.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 155	
ID	AEO43963 standard; protein; 234 AA.
PID	Human PRO polipeptide #33.
PN	US2003068755-AI.
PD	10-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 156	
ID	ADA77818 standard; protein; 234 AA.
PID	Human secreted/transmembrane protein (PRO) #33.
PN	US2003073180-AI.
PD	17-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 157	
ID	ABM24758 standard; protein; 234 AA.
PID	Human secreted polipeptide PRO1664, SEQ ID NO:66.
PN	US2003104539-AI.
PD	05-JUN-2003.
PA	
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 158	
ID	AEBO03026 standard; protein; 234 AA.
PID	Human secreted/transmembrane protein (PRO) #33.
PN	US2003036131-AI.
PD	20-FEB-2003.
PA	
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 159	
ID	AHR30282 standard; protein; 234 AA.
PID	Human secreted polipeptide PRO1664, SEQ ID NO:66.
PN	US2003040075-AI.
PD	27-FEB-2003.
PA	
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 160	
ID	ABM17196 standard; protein; 234 AA.
PID	Human secreted polipeptide PRO1664, SEQ ID NO:66.
PN	US2003054459-AI.
PD	20-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 161	
ID	ABR94942 standard; protein; 234 AA.
PID	Human secreted polipeptide PRO1664, SEQ ID NO:66.
PN	US2003044930-AI.
PD	06-MAR-2003.
PA	
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 162	
ID	ABR95247 standard; protein; 234 AA.
PID	Human secreted polipeptide PRO1664, SEQ ID NO:66.
PN	US2003040071-AI.
PD	27-FEB-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
RESULT 163	
ID	ADBI7071 standard; protein; 234 AA.
PID	Human transmembrane PRO polipeptide (Segid 14).
PN	US2003050462-AI.
PD	13-MAR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 6;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131; Length 234,
Query Match	100.0%; Score 1195; DB 6; Length 234,

Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 164			
ID ABO21485 standard; protein; 234 AA.			
DE Human secreted/transmembrane protein (PRO) #33.			
PN US2003054471-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 165			
ID ABR97749 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003064452-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 166			
ID ABR87537 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003068705-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 167			
ID ABR77578 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003054473-A1.			
PD 20-MAR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 168			
ID AAM27808 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003064440-A1.			
PD 03-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 169			
ID AAM06089 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003068704-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 170			
ID AAM03595 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003068722-A1.			
PD 10-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 171			
ID AAM35046 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003073183-A1.			
PD 17-APR-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 172			
ID AAM26283 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003104549-A1.			
PD 05-JUN-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 173			
ID AAM26283 standard; protein; 234 AA.			
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.			
PN US2003104549-A1.			
PD 05-JUN-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1195; DB 6;	Length 234
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;	
RESULT 173			



ID ABO48065 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 174  
ID ABR92807 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 175  
ID ABO24568 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 176  
ID ABO11579 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 177  
ID ABO2680 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 178  
ID ABO15976 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 179  
ID ABO27537 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 180  
ID ABO29028 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 181  
ID ABO7004 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 182  
ID ABO21098 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 183  
ID ABO9444 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 184  
ID ABO41314 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 185  
ID ABO36129 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 186  
ID ABO43658 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 187  
ID ABO76358 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 188  
ID ABO76054 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 189  
ID ABO25673 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 190  
ID ABO25978 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 191  
ID ABO03331 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 192  
ID ABO02416 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 193  
ID ABO44245 standard; protein; 234 AA.  
DE Human secreted/transmembrane polypeptide PRO 1864.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 194  
ID ABR90587 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 195  
ID ABR73655 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 196  
ID ABO16907 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 197  
ID ABR94332 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 198  
ID ABR75839 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 199  
ID ABR71215 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 200  
ID ABR93112 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 201  
ID ABR93417 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054478-A1.

PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 202  
ID ABR87842 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 203  
ID ABO27842 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 204  
ID ABO29977 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 205  
ID ABO33186 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 206  
ID ABO44874 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 207  
ID ABO8834 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 208  
ID ABO36434 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 209  
ID ABO35519 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 210  
ID ABO39484 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068776-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 211  
ID ABM10359 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 212  
ID ABM11884 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 213  
ID ABO52030 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003048768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 214  
ID ABO52335 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 215  
ID ABA19876 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 216  
ID ABO23653 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 217  
ID ADB17259 standard; protein; 234 AA.  
DE Human transmembrane PRO polypeptide (SeqID 14).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 218  
ID ABR97139 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 219  
ID ABR86927 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 220  
ID ABM10969 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 221  
ID ABM28113 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 222  
ID ABO32112 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 223  
ID ABM15239 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 224  
ID ABM06394 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 225  
ID ABM04205 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 226  
ID ABM22318 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 227  
ID ABM07614 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 228  
ID ABO40704 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
Query Match 100.0%; Score 1195; DB 6; Length 234;

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RESULT 229
ID AEM35351 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 230
ID AEM33114 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 231
ID ABO52640 standard; protein: 234 AA.
DE Human PRO polypeptide #33.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 232
ID ABO50200 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003048777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 233
ID ABU99194 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 234
ID ABO04246 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 235
ID ABO05876 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 236
ID AEM18416 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 237
ID ABR97444 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 238
ID ABR80544 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 239
ID AEM01155 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 240
ID ABR88757 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 241
ID AEM13409 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 242
ID ABK20793 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 243
ID ABO41924 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 244
ID ABO42534 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003048751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 245
ID AEM10054 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 246
ID ABO38569 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 247
ID AEM32809 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 267
ID ABO4334 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US200310061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 268
ID ABO20265 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 269
ID ABO21180 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 270
ID ABO22095 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 271
ID ADA20048 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 272
ID ABO34173 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 273
ID ABR96529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 274
ID ABR85707 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 275
ID ABR9689 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 276
ID ABO00545 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 277
ID ABO00240 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 278
ID ABO23672 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 279
ID ABO23538 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 280
ID ABO23933 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068799-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 281
ID ABO38264 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 282
ID ABO45564 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 283
ID ABO20488 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 284
ID ADA81337 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 285
ID ABO16602 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027276-A1.
PD 06-FEB-2003.
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Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 286  
ID ABO18228 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 287  
ID ABO22655 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 288  
ID ABO22960 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 289  
ID ABR92502 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 290  
ID ABR81459 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 291  
ID ABR77883 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 292  
ID ABR89672 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 293  
ID ABR26588 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US200303121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 294  
ID ABR13714 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 295  
ID ABO28452 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.

PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 296  
ID ABO30282 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 297  
ID ABO07309 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 298  
ID ABO03900 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 299  
ID ABO37044 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 300  
ID ABO41619 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 301  
ID ABO35214 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 302  
ID ABR25063 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 303  
ID ABO47455 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 304  
ID ABO47760 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049747-A1.  
PD 13-MAR-2003.



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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 305
ID ABO48370 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 306
ID ABO51420 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 307
ID ABO51725 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 308
ID ABO50505 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 309
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 310
ID ABM16891 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 311
ID ABO17923 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 312
ID ABO20875 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 313
ID ABR96834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 314
ID ABM12189 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 315
ID ABM16281 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 316
ID ABM24148 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 317
ID ABM14629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 318
ID ABM04510 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 319
ID ABM0669 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 320
ID ABM09139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 321
ID ABO39179 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 322
ID ABM75444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 323
ID ABM25368 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003104541-A1.
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PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 324
ID ABL19678 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 325
ID ABO46784 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 326
ID ABO47089 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 327
ID ADB83135 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 328
ID ABR71520 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 329
ID ABR72130 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 330
ID ABR98469 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 331
ID ABO06839 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 332
ID ABR84792 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 333
ID ABR73350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 334
ID ABR76444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 335
ID ABR73045 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 336
ID ABL18111 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 337
ID ABO20570 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 338
ID ABO25313 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 339
ID ABO25618 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 340
ID ABR94027 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 341
ID ABR79934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 342
ID ABL1274 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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RESULT 343  
ID ABO32881 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 344  
ID ABO30587 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 345  
ID ABO30892 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 346  
ID ABM27198 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 347  
ID ABM2943 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 348  
ID ABM05479 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 349  
ID ABM15544 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 350  
ID ABM08529 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 351  
ID ABO42229 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 352  
ID ABO00345 standard; protein; 234 AA.  
DE Human secreted/transmembrane polypeptide PRO 1864.

ID ABO37959 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 353  
ID ABO45869 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 354  
ID ABM6672 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 355  
ID ADB20178 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 356  
ID ABM19573 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 357  
ID ABO49285 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 358  
ID ABO49590 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 359  
ID ABO78430 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 360  
ID ABR88147 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 361  
ID ADA00345 standard; protein; 234 AA.  
DE Human secreted/transmembrane polypeptide PRO 1864.

PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 362  
ID AM26893 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 363  
ID AM003290 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 364  
ID ABO39789 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 365  
ID ABO49895 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 366  
ID ABO50810 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 367  
ID ABO05266 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 368  
ID ABR74570 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 369  
ID ABR77049 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 370  
ID ABR17806 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 371  
ID ABR95857 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 372  
ID ABO21790 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 373  
ID ABO19960 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 374  
ID ABO24263 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 375  
ID ABR86012 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 376  
ID ABR10664 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 377  
ID ABR76663 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 378  
ID ABR89367 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 379  
ID ABR12494 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 380  
ID ABR05784 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068717-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 381  
ID ABO34909 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 382  
ID ABM02985 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 383  
ID ABM18963 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 384  
ID ABM19268 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 385  
ID ABO46479 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 386  
ID ABO46980 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 387  
ID ABR69023 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 388  
ID ABR89062 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 389  
ID ABR72435 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 390  
ID ABR74265 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 391  
ID ABO18533 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 392  
ID ABR80239 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 393  
ID ABM01460 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 394  
ID ABM02070 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 395  
ID ABR87232 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 396  
ID ABM12799 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 397  
ID ABM30553 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 398  
ID ABM24453 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 399  
ID ABO29367 standard; protein; 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 400  
ID ABO31197 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 401  
ID ABM14324 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 402  
ID ABM09749 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 403  
ID ABO38874 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 404  
ID ABM34639 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 405  
ID ABO5115 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 406  
ID ABO03941 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 407  
ID ABO10411 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 408  
ID ABR77654 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 409  
ID ABR78864 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 410  
ID ABO23958 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 411  
ID ABR93722 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 412  
ID ABM01765 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 413  
ID ABM78188 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 414  
ID ABR8977 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 415  
ID ABM27503 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 416  
ID ABM13104 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 417  
ID ABO31807 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 418

ID ABO14019 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 419  
ID ABO18224 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068754-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 420  
ID ABO40094 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 421  
ID ABO74529 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 422  
ID ABO33724 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 423  
ID ABO20183 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 424  
ID ABO48675 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 425  
ID ABO72740 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 426  
ID ABO15382 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 427  
ID ABO85097 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040065-A1.  
PD 27-FEB-2003.

Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 428  
ID ABO15077 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 429  
ID ABO17212 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 430  
ID ABO17501 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 431  
ID ABO85402 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 432  
ID ABO76968 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 433  
ID ABO28147 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064459-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 434  
ID ABO22928 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068757-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 435  
ID ABO30248 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068723-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 436  
ID ABO21708 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068741-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 437  
ID ABO21403 standard; protein; 234 AA.



DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 438  
ID AM14934 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 439  
ID ABO41009 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 440  
ID ABO36739 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 441  
ID ABO37349 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 442  
ID AMW75139 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 443  
ID AAM33419 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 444  
ID ABO46174 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 445  
ID ADA82501 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 446  
ID ADB8587 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.

PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 447  
ID ABW31773 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 448  
ID ABM31163 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 449  
ID ADB85809 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 450  
ID ABM32078 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 451  
ID ABM32383 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 452  
ID ADB68266 standard; protein; 234 AA.  
DE Human PRO1864 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 453  
ID ADB68073 standard; protein; 234 AA.  
DE Human PRO1864 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 454  
ID ABM31468 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 455  
ID ABM30858 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068771-A1.  
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 456
ID ADB90890 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 457
ID ADC06970 standard; protein; 234 AA.
DE Human PRO1864 protein.
PD US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 458
ID ADC17149 standard; protein; 234 AA.
DE Mammalian PRO polypeptide (Seqid 14).
PD US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 459
ID ADC1847 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 460
ID ADC52342 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 461
ID ADD05539 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 462
ID ADD10351 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PD US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 463
ID ADD11311 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PD US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 464
ID ADD37104 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PD US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 465
ID ADD36018 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 466
ID ADG01019 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 467
ID ADG08572 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 468
ID ADG02534 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 469
ID ADG01241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 470
ID ADF95416 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 471
ID ADF95193 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 472
ID ADG12231 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 473
ID ADH24046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PD US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

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RESULT 474  
ID ADH34072 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 475  
ID ADH29905 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 476  
ID ADH2376 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 477  
ID ADH08891 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 478  
ID ADG8580 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 479  
ID ADH2456 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 480  
ID ADH37412 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 481  
ID ADH02001 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 482  
ID ADH37582 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 483

ID ADG85620 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 484  
ID ADH24216 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 485  
ID ADH38510 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 486  
ID ADG83631 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 487  
ID ADH29439 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 488  
ID ADH2755 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 489  
ID ADH37752 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 490  
ID ADH37929 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 491  
ID ADH57349 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 492  
ID ADH53491 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 493  
ID ADH53661 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 494  
ID ADH51997 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 495  
ID ADH48852 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 496  
ID ADI25362 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 497  
ID ADH90155 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 498  
ID ADI25532 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 499  
ID ADH9706 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 500  
ID ADI03554 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 501  
ID ADI11911 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 502  
ID ADH89985 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 503  
ID ADH98386 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 504  
ID ADI11061 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 505  
ID ADI11571 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 506  
ID ADH98216 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 507  
ID ADH98556 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 508  
ID ADH98046 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 509  
ID ADI05034 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 510  
ID ADI03384 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181654-A1.

PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 511	
ID	AD104779 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PN	US2003181657-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 512	
ID	ADH78233 standard; protein; 234 AA.
DE	Human PRO polypeptide #7.
PN	US2003181658-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 513	
ID	ADI19577 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PN	US2003181676-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 514	
ID	ADH90325 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PN	US2003181699-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 515	
ID	ADI03044 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PN	US2003181653-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 516	
ID	ADH77893 standard; protein; 234 AA.
DE	Human PRO polypeptide #7.
PN	US2003181666-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 517	
ID	ADH97876 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PN	US2003181674-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 518	
ID	ADI01261 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PN	US2003190669-A1.
PD	09-OCT-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1195; DB 7; Length 234;
Beet Local Similarity	100.0%; Pred. No. 1.3e-131,
RESULT 519	
ID	ADI01956 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PN	US2003181652-A1.
PD	25-SEP-2003.

PA	(GETH ) GENENTECH INC.	100.0%;	Score 1195;	DB 7;	Length 234;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 520					
ID	AD103224 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
PN	US2003181655-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 521					
ID	AD111401 standard; protein; 234 AA.				
DE	Human PRO polypeptide #7.				
PN	US2003181681-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 523					
ID	AD111741 standard; protein; 234 AA.				
DE	Human PRO polypeptide #7.				
PN	US2003181685-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 524					
ID	AD105378 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
PN	US2003190716-A1.				
PD	09-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 525					
ID	ADH79450 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
PN	US2003191290-A1.				
PD	09-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 526					
ID	AD119407 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
PN	US2003181675-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 527					
ID	AD105208 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
PN	US2003181677-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 528					
ID	ADH79620 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
PN	US2003191286-A1.				
PD	09-OCT-2003.				
PA	(GETH ) GENENTECH INC.				

Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 529				
ID ADI01446 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003181678-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 530				
ID ADI01616 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003181679-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 531				
ID ADI01766 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003181680-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 532				
ID ADH79790 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003191289-A1.				
PD 09-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 533				
ID ADI04608 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003171550-A1.				
PD 11-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 534				
ID ADI02744 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003181651-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 535				
ID ADH78063 standard; protein; 234 AA.				
DE Human PRO polypeptide #7.				
PN US2003181667-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 536				
ID ADI25702 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003181670-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
RESULT 537				
ID ADI55872 standard; protein; 234 AA.				
DE Novel1 human secreted and transmembrane protein PRO1864.				
PN US2003181671-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131,		
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;

Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 538		
ID ADK65384 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
PN US2003073821-A1.		
PD 17-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 539		
ID ADH98726 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
PN US2003191284-A1.		
PD 09-OCT-2003		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 540		
ID ADH79967 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
PN US2003191287-A1.		
PD 09-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 541		
ID ADL32672 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
PN US2003207396-A1.		
PD 06-NOV-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 542		
ID ADM30206 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
PN US2003073813-A1.		
PD 17-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 543		
ID ADL33698 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
PN US2003040013-A1.		
PD 27-FEB-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 544		
ID ADC52152 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
PN US2003130483-A1.		
PD 10-JUL-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 545		
ID ADK41312 standard; protein; 234 AA.		
DE Human secreted/transmembrane PRO polypeptide #31.		
PN US2003100457-A1.		
PD 29-MAY-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 546		
ID ADE74203 standard; protein; 234 AA.		
DE Human secreted/transmembrane protein (PRO) #33.		
PN US2003211572-A1.		
PD 13-NOV-2003.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;
RESULT 547		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.3e-131;

ID AD874815 standard; protein; 234 AA.  
DE Human secreted/cransmembrane protein (PRO) #33.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 548  
ID ADF96028 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 549  
ID ADG04299 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 550  
ID ADG00459 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 551  
ID ADH06584 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 552  
ID ADH06414 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 553  
ID ADG68635 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 554  
ID ADH27725 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 555  
ID ADH25066 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 556  
ID ADH33698 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181645-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 557  
ID ADG82715 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 558  
ID ADH02341 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 559  
ID ADH07948 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 560  
ID ADG69345 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 561  
ID ADH39166 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 562  
ID ADH25996 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003068770-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 563  
ID ADG83906 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 564  
ID ADG85450 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 565  
ID ADH06244 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180854-A1.  
PD 25-SEP-2003.



[illegible]

Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 575				
ID	ADH01078	standard; protein; 234 AA.		
DE	Human PRO polypeptide #7.			
FN	US2003180638-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 576				
ID	ADG69685	standard; protein; 234 AA.		
DE	Novel human secreted and transmembrane protein PRO1864.			
FN	US2003180843-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 577				
ID	ADH02171	standard; protein; 234 AA.		
DE	Human PRO polypeptide #7.			
FN	US2003180841-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 578				
ID	ADG69175	standard; protein; 234 AA.		
DE	Novel human secreted and transmembrane protein PRO1864.			
FN	US2003180847-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 579				
ID	ADG85960	standard; protein; 234 AA.		
DE	Novel human secreted and transmembrane protein PRO1864.			
FN	US2003180862-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 580				
ID	ADH24896	standard; protein; 234 AA.		
DE	Novel human secreted and transmembrane protein PRO1864.			
FN	US2003180909-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 581				
ID	ADH39513	standard; protein; 234 AA.		
DE	Novel human secreted and transmembrane protein PRO1864.			
FN	US2003180915-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 582				
ID	ADH02511	standard; protein; 234 AA.		
DE	Human PRO polypeptide #7.			
FN	US2003180840-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
RESULT 583				
ID	ADG69005	standard; protein; 234 AA.		
DE	Novel human secreted and transmembrane protein PRO1864.			
FN	US2003180849-A1.			
PD	25-SEP-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Best Local Similarity	100.0%	Pred. No.1.3e-131;		
Query Match	100.0%	Score 1195;	DB 8;	Length 234;
Query Match	100.0%	Score 1195;	DB 8;	Length 234;

Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 584		
ID	ADH07608 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180850-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 585		
ID	ADG68130 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180863-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 586		
ID	ADH24726 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180908-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 587		
ID	ADH25774 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180911-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 588		
ID	ADH38340 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180922-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 589		
ID	ADH51719 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003181642-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 590		
ID	ADH43495 standard; protein; 234 AA.	
DE	Human PRO polypeptide #31.	
PN	US2003224984-A1.	
PD	04-DEC-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 591		
ID	ADH52167 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180921-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 592		
ID	ADH49533 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180857-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 593		
ID	ADH49533 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180857-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;

RESULT 593	ID	ADH90495	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003181700-A1.		
	PD	25-SEP-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 594	ID	AD11231	standard; protein; 234 AA.	
	DE	Human PRO polypeptide #7.		
	PN	US2003181683-A1.		
	PD	25-SEP-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 595	ID	ADH98896	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003190698-A1.		
	PD	09-OCT-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 596	ID	AD102126	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003190699-A1.		
	PD	09-OCT-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 597	ID	ADH90665	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003181701-A1.		
	PD	25-SEP-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 598	ID	ADJ54704	standard; protein; 234 AA.	
	DE	Human PRO polypeptide #33.		
	PN	US2004023321-A1.		
	PD	05-FEB-2004.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 599	ID	ADJ98540	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003187197-A1.		
	PD	02-OCT-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 600	ID	ADJ98710	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003187228-A1.		
	PD	02-OCT-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 601	ID	ADH78869	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003181703-A1.		
	PD	25-SEP-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 602	ID	ADH78869	standard; protein; 234 AA.	
	DE	Novel1	human secreted and transmembrane protein PRO1864.	
	PN	US2003181703-A1.		
	PD	25-SEP-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		100.0%;	Score 1195; DB 8; Length 234;
	Best Local Similarity		100.0%;	Pred. No. 1.3e-131;

ID ADJ99103 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 603  
ID ADJ99273 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 604  
ID ADJ98891 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 605  
ID ADH79039 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 606  
ID ADK00899 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 607  
ID ADK14420 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 608  
ID ADK82840 standard; protein; 234 AA.  
DE Human PRO polypeptide #31.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 609  
ID ADJ64475 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2004036337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 610  
ID ADM31371 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 611  
ID ADM36418 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 612  
ID ADM40223 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 613  
ID ADM80869 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 614  
ID ADL91873 standard; protein; 234 AA.  
DE Human PRO1864 protein SEQ ID NO:94.  
PN WO2004024076-A2.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 615  
ID ADN37831 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2004051959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
RESULT 616  
ID AAM41716 standard; protein; 238 AA.  
DE Human polypeptide SEQ ID NO 6647.  
PN WO20015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 100.0%; Score 1195; DB 4; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.4e-131;  
RESULT 617  
ID AAM41715 standard; protein; 238 AA.  
DE Human polypeptide SEQ ID NO 6646.  
PN WO20015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 100.0%; Score 1195; DB 4; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.4e-131;  
RESULT 618  
ID ABP75508 standard; protein; 238 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 692.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 100.0%; Score 1195; DB 6; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.4e-131;  
RESULT 619  
ID ABR58404 standard; protein; 234 AA.  
DE Human NOV19D.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 99.4%; Score 1188; DB 6; Length 234;  
Best Local Similarity 99.6%; Pred. No. 8.9e-131;  
RESULT 620  
ID AAM39930 standard; protein; 216 AA.  
DE Human polypeptide SEQ ID NO 3075.

PN W0200153312-A1.  
ID 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 91.8%; Score 1097; DB 4; Length 216;  
Best Local Similarity 92.3%; Pred. No. 4.1e-120;  
RESULT 621  
ID ABB90287 standard; protein; 201 AA.  
DE Human polypeptide SEQ ID NO 2663.  
PN W0200150304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 85.7%; Score 1024; DB 5; Length 201;  
Best Local Similarity 100.0%; Pred. No. 1.4e-111;  
RESULT 622  
ID ABB58403 standard; protein; 198 AA.  
DE Human NOV19a.  
PN W02003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 82.4%; Score 985; DB 6; Length 198;  
Best Local Similarity 84.6%; Pred. No. 5.4e-107;  
RESULT 623  
ID AAN30250 standard; protein; 283 AA.  
DE Novel human secreted protein #741.  
PN W0200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 65.0%; Score 777; DB 4; Length 283;  
Best Local Similarity 72.5%; Pred. No. 2.6e-82;  
RESULT 624  
ID ADB64413 standard; protein; 176 AA.  
DE Human protein encoded by clone FEBRA20007820.  
PN EP108459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
Query Match 55.0%; Score 669.5; DB 7; Length 176;  
Best Local Similarity 87.5%; Pred. No. 6e-70;  
RESULT 625  
ID ADK36828 standard; protein; 146 AA.  
DE Novel human polypeptide SeqID8910.  
PN W0200216439-A2.  
PD 28-FEB-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 55.6%; Score 665; DB 5; Length 146;  
Best Local Similarity 91.0%; Pred. No. 1.6e-69;  
RESULT 626  
ID AAM25768 standard; protein; 445 AA.  
DE Human MLN 64.  
PN W03706256-A2.  
PD 20-FEB-1997.  
PA (INRM) INST NAT SANTE & RECH MEDICALE.  
PA (CNRS) CENT NAT RECH SCI.  
PA (UTPA-) UNIV PASTEUR LOUIS.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 55.6%; Score 664; DB 2; Length 445;  
Best Local Similarity 56.2%; Pred. No. 9.6e-69;  
RESULT 627  
ID ABR47530 standard; protein; 445 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:296.  
PN W0200304989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 55.6%; Score 664; DB 6; Length 445;  
Best Local Similarity 56.2%; Pred. No. 9.6e-69;  
RESULT 628  
ID ADH13184 standard; protein; 445 AA.  
DE Human malignant neoplasia-related protein SeqID33.  
PN EP1365034-A2.  
PD 26-NOV-2003.  
PA (FARB) BAYER AG.  
Query Match 55.6%; Score 664; DB 8; Length 445;  
Best Local Similarity 56.2%; Pred. No. 9.6e-69;

RESULT 629  
ID ABB05498 standard; protein; 534 AA.  
DE Novel human diagnostic protein #5489.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 52.3%; Score 625; DB 4; Length 534;  
Best Local Similarity 48.9%; Pred. No. 4.8e-64;  
RESULT 630  
ID ABR69622 standard; protein; 412 AA.  
DE Human CGPD-22 protein.  
PN W02003027263-A2.  
PD 03-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 48.4%; Score 578; DB 6; Length 412;  
Best Local Similarity 58.3%; Pred. No. 1.1e-58;  
RESULT 631  
ID ABB75900 standard; protein; 111 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 1084.  
PN W0200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 33.9%; Score 405.5; DB 6; Length 111;  
Best Local Similarity 73.7%; Pred. No. 3.6e-39;  
RESULT 632  
ID ABB59968 standard; protein; 580 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6696.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 28.7%; Score 343; DB 4; Length 580;  
Best Local Similarity 37.8%; Pred. No. 8e-31;  
RESULT 633  
ID AAM90384 standard; protein; 70 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:17977.  
PN W0200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 26.9%; Score 322; DB 4; Length 70;  
Best Local Similarity 98.4%; Pred. No. 1.3e-29;  
RESULT 634  
ID AAB96637 standard; protein; 424 AA.  
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Query Match 7.8%; Score 93.5; DB 4; Length 424;  
Best Local Similarity 21.9%; Pred. No. 0.12;  
RESULT 635  
ID AAU03699 standard; protein; 373 AA.  
DE Group B streptococcus antigenic protein, ID-176.  
PN W0200132882-A2.  
PD 10-MAY-2001.  
PA (MICR-) MICROBIAL TECHNIQS LTD.  
Query Match 7.6%; Score 91; DB 4; Length 373;  
Best Local Similarity 25.7%; Pred. No. 0.19;  
RESULT 636  
ID ABB30317 standard; protein; 651 AA.  
DE Streptococcus polypeptide SEQ ID NO 9810.  
PN W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 7.6%; Score 91; DB 5; Length 651;  
Best Local Similarity 25.7%; Pred. No. 0.42;  
RESULT 637  
ID ABB29732 standard; protein; 654 AA.  
DE Streptococcus polypeptide SEQ ID NO 8640.  
PN W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.

Query Match 7.6%; Score 91; DB 5; Length 654;  
Best Local Similarity 25.7%; Pred. No. 0.42;  
RESULT 638  
ID ABB26469 standard; protein; 654 AA.  
DE Streptococcus polypeptide SEQ ID NO 2114.  
PN W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 7.6%; Score 91; DB 5; Length 654;  
Best Local Similarity 25.7%; Pred. No. 0.42;  
RESULT 639  
ID AAG61678 standard; protein; 155 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 7.3%; Score 87.5; DB 3; Length 155;  
Best Local Similarity 21.4%; Pred. No. 0.15;  
RESULT 640  
ID AAG59838 standard; protein; 155 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 7.3%; Score 87.5; DB 3; Length 155;  
Best Local Similarity 21.4%; Pred. No. 0.15;  
RESULT 641  
ID AAB58945 standard; protein; 516 AA.  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.  
PN W0200055173-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.3%; Score 87.5; DB 3; Length 516;  
Best Local Similarity 25.2%; Pred. No. 0.78;  
RESULT 642  
ID ADO39266 standard; protein; 421 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 929.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.3%; Score 87; DB 8; Length 421;  
Best Local Similarity 23.7%; Pred. No. 0.67;  
RESULT 643  
ID ADO39263 standard; protein; 223 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 926.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 223;  
Best Local Similarity 25.5%; Pred. No. 0.42;  
RESULT 644  
ID ADO39258 standard; protein; 285 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 921.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 285;  
Best Local Similarity 25.5%; Pred. No. 0.53;  
RESULT 645  
ID ADO39262 standard; protein; 315 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 925.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 315;  
Best Local Similarity 25.5%; Pred. No. 0.68;  
RESULT 646  
ID ADO39260 standard; protein; 323 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 923.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 323;  
Best Local Similarity 25.5%; Pred. No. 0.7;

RESULT 647  
ID ADO39261 standard; protein; 328 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 924.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 328;  
Best Local Similarity 25.5%; Pred. No. 0.71;  
RESULT 648  
ID ADO39265 standard; protein; 338 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 928.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 338;  
Best Local Similarity 25.5%; Pred. No. 0.74;  
RESULT 649  
ID ADO39267 standard; protein; 339 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 930.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 339;  
Best Local Similarity 25.5%; Pred. No. 0.75;  
RESULT 650  
ID ADE28099 standard; protein; 340 AA.  
DE Human NTRAN protein - SEQ ID 4.  
PN W02003051902-A1.  
PD 26-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.2%; Score 85.5; DB 7; Length 340;  
Best Local Similarity 25.5%; Pred. No. 0.75;  
RESULT 651  
ID ADO39269 standard; protein; 384 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 932.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 384;  
Best Local Similarity 25.5%; Pred. No. 0.89;  
RESULT 652  
ID ADO39264 standard; protein; 390 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 927.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 390;  
Best Local Similarity 25.5%; Pred. No. 0.91;  
RESULT 653  
ID ABU26680 standard; protein; 396 AA.  
DE Protein encoded by Prokaryotic essential gene #12207.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.2%; Score 85.5; DB 6; Length 396;  
Best Local Similarity 21.0%; Pred. No. 0.93;  
RESULT 654  
ID AAM13575 standard; protein; 438 AA.  
DE Batten disease polypeptide CLN3.  
PN W09708308-A1.  
PD 06-MAR-1997.  
PA (GENO-) GEN HOSPITAL CORP.  
PA (UYLR-) RIKSUNIV LEIDEN.  
Query Match 7.2%; Score 85.5; DB 2; Length 438;  
Best Local Similarity 25.5%; Pred. No. 1.1;  
RESULT 655  
ID AAM13589 standard; protein; 438 AA.  
DE Batten disease CLN3 mutant protein in family L204.  
PN W09708308-A1.  
PD 06-MAR-1997.  
PA (GENO-) GEN HOSPITAL CORP.  
PA (UYLR-) RIKSUNIV LEIDEN.  
Query Match 7.2%; Score 85.5; DB 2; Length 438;

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Best Local Similarity 24.8%; Pred. No. 1.1;
RESULT 656
ID AAW13582 standard; protein; 438 AA.
DE Batten disease Cln3 mutant protein in family L46.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UTLE-) RIJXSUNIV LEIDEN.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 2; Length 438;
RESULT 657
ID AAW13577 standard; protein; 438 AA.
DE Batten disease Cln3 mutant protein in family L39.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UTLE-) RIJXSUNIV LEIDEN.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 2; Length 438;
RESULT 658
ID AD096392 standard; protein; 438 AA.
DE T cell activation associated protein #285.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 438;
RESULT 659
ID AD039268 standard; protein; 438 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 438;
RESULT 660
ID ADA05822 standard; protein; 440 AA.
DE Human NOV43a protein SEQ ID NO:182.
PN W02003029424-A2.
PD 10-APR-2003.
PA (CIRA-) CIRA GEN CORP.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 6; Length 440;
RESULT 661
ID ADM63244 standard; protein; 440 AA.
DE Human NOV43a variant.
PN U62004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUTU/) JU J.
PA (LILU/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (ZERN/) ZERHUSEN B D.
PA (AND/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
Best Local Similarity 25.5%; Pred. No. 1.1;
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 440;
RESULT 662
ID ADN62985 standard; protein; 440 AA.
DE Human NOV43a.
PN U62004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUTU/) JU J.
PA (LILU/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERN/) ZERHUSEN B D.
PA (AND/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 440;
RESULT 663
ID AAW13593 standard; protein; 467 AA.
DE Batten disease Cln3 mutant protein in family L61.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UTLE-) RIJXSUNIV LEIDEN.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 2; Length 467;
RESULT 664
ID ABB89640 standard; protein; 473 AA.
DE Human polypeptide SEQ ID NO 2016.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.2%; Score 85.5; DB 5; Length 473;
RESULT 665
ID ADQ18055 standard; protein; 473 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN W02004048938-A2.
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PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.2%; Score 85.5; DB 8; Length 473;  
Best Local Similarity 25.2%; Pred. No. 1.2;  
RESULT 666  
ID AB040544 standard; protein; 500 AA.  
DE Protein encoded by Prokaryotic essential gene #26071.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 7.2%; Score 85.5; DB 6; Length 500;  
Best Local Similarity 26.0%; Pred. No. 1.3;  
RESULT 667  
ID AB033210 standard; protein; 430 AA.  
DE Protein encoded by Prokaryotic essential gene #18737.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 7.1%; Score 84.5; DB 6; Length 430;  
Best Local Similarity 25.5%; Pred. No. 1.4;  
RESULT 668  
ID AAM13588 standard; protein; 438 AA.  
DE Bacten disease CLN3 mutant protein in family L10.  
PN W09708308-A1.  
PD 06-MAR-1997.  
PA (GEHO-) GEN HOSPITAL CORP.  
Query Match 7.1%; Score 84.5; DB 2; Length 438;  
Best Local Similarity 24.8%; Pred. No. 1.4;  
RESULT 669  
ID AAG16921 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17749.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.0%; Score 83.5; DB 3; Length 322;  
Best Local Similarity 33.7%; Pred. No. 1.2;  
RESULT 670  
ID ABG21285 standard; protein; 472 AA.  
DE Novel human diagnostic protein #21276.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 83.5; DB 4; Length 472;  
Best Local Similarity 20.1%; Pred. No. 2;  
RESULT 671  
ID AB035608 standard; protein; 239 AA.  
DE Protein encoded by Prokaryotic essential gene #21135.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 6.9%; Score 82.5; DB 6; Length 239;  
Best Local Similarity 21.7%; Pred. No. 1;  
RESULT 672  
ID AAM13590 standard; protein; 438 AA.  
DE Bacten disease CLN3 mutant protein in family L216.  
PN W09708308-A1.  
PD 06-MAR-1997.  
PA (GEHO-) GEN HOSPITAL CORP.  
Query Match 6.9%; Score 82.5; DB 2; Length 438;  
Best Local Similarity 24.8%; Pred. No. 2.4;  
RESULT 673  
ID ADB85263 standard; protein; 589 AA.  
DE Mouse RNAI homologue SEQ ID NO:144.  
PN EP1284297-A2.  
PD 19-FEB-2003.  
PA (WARN-) WARNER LAMBERT CO.  
Query Match 6.9%; Score 82; DB 7; Length 589;  
Best Local Similarity 19.5%; Pred. No. 4.2;  
RESULT 674  
ID AAM13586 standard; protein; 438 AA.  
DE Bacten disease CLN3 mutant protein in family L285.  
PN W09708308-A1.

PD 06-MAR-1997.  
PA (GEHO-) GEN HOSPITAL CORP.  
Query Match 6.8%; Score 81.5; DB 2; Length 438;  
Best Local Similarity 24.8%; Pred. No. 3.2;  
RESULT 675  
ID AAB92924 standard; protein; 519 AA.  
DE Human protein sequence SEQ ID NO:11574.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 6.8%; Score 81.5; DB 4; Length 519;  
Best Local Similarity 22.6%; Pred. No. 4;  
RESULT 676  
ID ADE28193 standard; protein; 577 AA.  
DE Human MDT protein - SEQ ID 43.  
PN W02003046152-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.8%; Score 81.5; DB 7; Length 577;  
Best Local Similarity 22.6%; Pred. No. 4.6;  
RESULT 677  
ID ADN23155 standard; protein; 529 AA.  
DE Bacterial polypeptide #5808.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SIAT-) SIATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match 6.8%; Score 81; DB 8; Length 529;  
Best Local Similarity 23.1%; Pred. No. 4.7;  
RESULT 678  
ID ADN23156 standard; protein; 529 AA.  
DE Bacterial polypeptide #5809.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SIAT-) SIATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match 6.8%; Score 81; DB 8; Length 529;  
Best Local Similarity 23.1%; Pred. No. 4.7;  
RESULT 679  
ID AAG53771 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68491.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 80.5; DB 3; Length 322;  
Best Local Similarity 32.7%; Pred. No. 2.7;  
RESULT 680  
ID AAG25639 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29783.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 80.5; DB 3; Length 322;  
Best Local Similarity 32.7%; Pred. No. 2.7;  
RESULT 681  
ID AAG53746 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68457.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 80.5; DB 3; Length 322;  
Best Local Similarity 32.7%; Pred. No. 2.7;  
RESULT 682  
ID ABO63194 standard; protein; 350 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9711.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.7%; Score 80.5; DB 7; Length 350;



Best Local Similarity 31.8%; Pred. No. 3;  
RESULT 683  
ID ABB48552 standard; protein; 463 AA.  
DE Ilisteria monocytogenes protein #1256.  
PN W0200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match 6.7%; Score 80.5; DB 5; Length 463;  
Best Local Similarity 19.0%; Pred. No. 4.5;  
RESULT 684  
ID ABB31036 standard; protein; 463 AA.  
DE Protein encoded by prokaryotic essential gene #16563.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.7%; Score 80.5; DB 6; Length 463;  
Best Local Similarity 19.0%; Pred. No. 4.5;  
RESULT 685  
ID ADD43670 standard; protein; 536 AA.  
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 165.  
PN W02003049762-A2.  
PD 19-JUN-2003.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.7%; Score 80.5; DB 7; Length 536;  
Best Local Similarity 25.2%; Pred. No. 5.5;  
RESULT 686  
ID AOC42920 standard; protein; 891 AA.  
DE Vaccinia Virus Major Core protein Paa precursor.  
PN W02003017943-A2.  
PD 06-MAR-2003.  
PA (MYRI-) MYRIAD GENETICS INC.  
Query Match 6.7%; Score 80.5; DB 7; Length 891;  
Best Local Similarity 23.3%; Pred. No. 11;  
RESULT 687  
ID ABB92830 standard; protein; 1780 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2041.  
PN W0200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match 6.7%; Score 80.5; DB 5; Length 1780;  
Best Local Similarity 20.8%; Pred. No. 29;  
RESULT 688  
ID AAB54399 standard; protein; 144 AA.  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:851.  
PN W0200055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 80; DB 3; Length 144;  
Best Local Similarity 25.4%; Pred. No. 1;  
RESULT 689  
ID AAM39952 standard; protein; 238 AA.  
DE Human polypeptide SEQ ID NO 3097.  
PN W0200153112-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.7%; Score 80; DB 4; Length 238;  
Best Local Similarity 22.5%; Pred. No. 2;  
RESULT 690  
ID ADM04473 standard; protein; 238 AA.  
DE Human protein of the invention SEQ ID NO:3158.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.7%; Score 80; DB 7; Length 238;  
Best Local Similarity 22.5%; Pred. No. 2;  
RESULT 691  
ID AAM41738 standard; protein; 249 AA.  
DE Human polypeptide SEQ ID NO 6669.  
PN W0200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.7%; Score 80; DB 4; Length 249;  
Best Local Similarity 22.5%; Pred. No. 2.2;

RESULT 692  
ID AAR77844 standard; protein; 309 AA.  
DE Molasses toxicity resistance protein RTM1.  
PN W09514774-A2.  
PD 01-JUN-1995.  
PA (CNRS) CENT NAT RECH SCI.  
Query Match 6.7%; Score 80; DB 2; Length 309;  
Best Local Similarity 28.0%; Pred. No. 2.9;  
RESULT 693  
ID AAB67388 standard; protein; 330 AA.  
DE Photorhabdus luminescens protein sequence #485.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 6.7%; Score 80; DB 6; Length 330;  
Best Local Similarity 24.6%; Pred. No. 3.2;  
RESULT 694  
ID AAB03831 standard; protein; 360 AA.  
DE Human gene 14 encoded secreted protein HDGFN31, SEQ ID NO: 77.  
PN W0200136440-A1.  
PD 25-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 80; DB 4; Length 360;  
Best Local Similarity 22.5%; Pred. No. 3.6;  
RESULT 695  
ID ABB64559 standard; protein; 360 AA.  
DE Human albumin fusion protein #1234.  
PN W0200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 80; DB 5; Length 360;  
Best Local Similarity 22.5%; Pred. No. 3.6;  
RESULT 696  
ID ADL77826 standard; protein; 360 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1308.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 6.7%; Score 80; DB 8; Length 360;  
Best Local Similarity 22.5%; Pred. No. 3.6;  
RESULT 697  
ID ABB25554 standard; protein; 365 AA.  
DE Protein encoded by prokaryotic essential gene #11081.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.7%; Score 79.5; DB 6; Length 365;  
Best Local Similarity 21.2%; Pred. No. 4.2;  
RESULT 698  
ID AAR58703 standard; protein; 406 AA.  
DE HCMV IE-exon-4 subunit.  
PN W09417810-A1.  
PD 18-AUG-1994.  
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
Query Match 6.7%; Score 79.5; DB 2; Length 406;  
Best Local Similarity 19.3%; Pred. No. 4.9;  
RESULT 699  
ID AAM27275 standard; protein; 406 AA.  
DE Human cytomagalovirus immediate-early exon 4 product.  
PN W09740165-A1.  
PD 30-OCT-1997.  
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
Query Match 6.7%; Score 80; DB 2; Length 406;  
Best Local Similarity 19.3%; Pred. No. 4.9;  
RESULT 700  
ID ABB58483 standard; protein; 638 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2241.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.7%; Score 79.5; DB 4; Length 638;

Best Local Similarity 20.5%; Pred. No. 9.1;  
 RESULT 701  
 ID ABE13277 standard; protein; 723 AA.  
 DE Human transporters and ion channels (TRICH)-4.  
 PN W0200177174-A2.  
 PD 18-OCT-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 6.7%; Score 79.5; DB 5; Length 723;  
 Best Local Similarity 18.0%; Pred. No. 11;  
 RESULT 702  
 ID ADL12774 standard; protein; 723 AA.  
 DE Human steroid-induced C3A liver cell protein #80.  
 PN U6673549-B1.  
 PD 06-JAN-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 6.7%; Score 79.5; DB 8; Length 723;  
 Best Local Similarity 18.0%; Pred. No. 11;  
 RESULT 703  
 ID AAW20696 standard; protein; 121 AA.  
 DE H. pylori secreted or periplasmic protein 05ae20220orf50.  
 PN W09640893-A1.  
 PD 19-DEC-1996.  
 PA (ASTR-) ASTRA AB.  
 Query Match 6.6%; Score 79; DB 2; Length 121;  
 Best Local Similarity 21.4%; Pred. No. 1;  
 RESULT 704  
 ID ABB60462 standard; protein; 323 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 8178.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Query Match 6.6%; Score 79; DB 4; Length 323;  
 Best Local Similarity 18.8%; Pred. No. 4.1;  
 RESULT 705  
 ID ABR58610 standard; protein; 1531 AA.  
 DE Human cancer related protein SEQ ID NO:267.  
 PN W02003025138-A2.  
 PD 27-MAR-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 6.6%; Score 79; DB 6; Length 1531;  
 Best Local Similarity 24.3%; Pred. No. 35;  
 RESULT 706  
 ID ADE31753 standard; protein; 1531 AA.  
 DE Human 59590 protein #SEQ ID 110.  
 PN W02003065984-A2.  
 PD 14-AUG-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 6.6%; Score 79; DB 7; Length 1531;  
 Best Local Similarity 24.3%; Pred. No. 35;  
 RESULT 707  
 ID ABU62069 standard; protein; 1597 AA.  
 DE Human heart alpha-kinase (HK).  
 PN U52002177205-A1.  
 PD 28-NOV-2002.  
 PA (RYAZ-) RYAZANOV A.  
 Query Match 6.6%; Score 79; DB 6; Length 1597;  
 Best Local Similarity 24.3%; Pred. No. 37;  
 RESULT 708  
 ID ABU62070 standard; protein; 1597 AA.  
 DE Mouse heart alpha-kinase (HK).  
 PN U52002177205-A1.  
 PD 28-NOV-2002.  
 PA (RYAZ-) RYAZANOV A.  
 Query Match 6.6%; Score 79; DB 6; Length 1597;  
 Best Local Similarity 24.3%; Pred. No. 37;  
 RESULT 709  
 ID ABO55689 standard; protein; 135 AA.  
 DE Human genome derived single exon protein #1923.  
 PN U62003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN-) PENN S G.  
 PA (RANK-) RANK D R.  
 PA (HANZ-) HANZEL D K.

Query Match 6.6%; Score 78.5; DB 8; Length 135;  
 Best Local Similarity 59.4%; Pred. No. 1.4;  
 RESULT 710  
 ID ADB10616 standard; protein; 228 AA.  
 DE Altolococcus ocellis antigenic protein SEQ ID NO:4244.  
 PN W02003048304-A2.  
 PD 12-JUN-2003.  
 PA (AMHP-) MYERH HOLDINGS CORP.  
 Query Match 6.6%; Score 78.5; DB 6; Length 228;  
 Best Local Similarity 22.5%; Pred. No. 2.9;  
 RESULT 711  
 ID ABU36298 standard; protein; 239 AA.  
 DE Protein encoded by Prokaryotic essential gene #21825.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELITR-) ELITRA PHARM INC.  
 Query Match 6.6%; Score 78.5; DB 6; Length 239;  
 Best Local Similarity 23.4%; Pred. No. 3.1;  
 RESULT 712  
 ID ADJ27174 standard; protein; 626 AA.  
 DE Human TRICH-6, SEQ ID 6.  
 PN W02004013293-A2.  
 PD 12-FEB-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 6.6%; Score 78.5; DB 8; Length 626;  
 Best Local Similarity 18.0%; Pred. No. 12;  
 RESULT 713  
 ID ABW84679 standard; protein; 648 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:5128.  
 PN W02004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 6.6%; Score 78.5; DB 8; Length 648;  
 Best Local Similarity 18.0%; Pred. No. 12;  
 RESULT 714  
 ID APM84877 standard; protein; 668 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:5126.  
 PN W02004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 6.6%; Score 78.5; DB 8; Length 668;  
 Best Local Similarity 18.0%; Pred. No. 13;  
 RESULT 715  
 ID ABP29904 standard; protein; 669 AA.  
 DE Streptococcus polypeptide SEQ ID NO 8984.  
 PN W0200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Query Match 6.6%; Score 78.5; DB 5; Length 669;  
 Best Local Similarity 23.5%; Pred. No. 13;  
 RESULT 716  
 ID ABP28724 standard; protein; 669 AA.  
 DE Streptococcus polypeptide SEQ ID NO 6624.  
 PN W0200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Query Match 6.6%; Score 78.5; DB 5; Length 669;  
 Best Local Similarity 23.5%; Pred. No. 13;  
 RESULT 717  
 ID ADJ21047 standard; protein; 703 AA.  
 DE Novel human protein #22.  
 PN W02003025148-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 6.6%; Score 78.5; DB 7; Length 703;  
 Best Local Similarity 18.0%; Pred. No. 14;  
 RESULT 718  
 ID ABW84682 standard; protein; 711 AA.  
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:5131.  
 PN W02004023973-A2.  
 PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.  
 Query Match 6.6%; Score 78.5; DB 8; Length 711;  
 Best Local Similarity 18.0%; Pred. No. 14;  
 RESULT 719  
 ID ABB52105 standard; protein; 723 AA.  
 DE Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.  
 PN EP1217066-A1.  
 PD 26-JUN-2002.  
 PA (UYGE-) UNIV GENT.  
 Query Match 6.6%; Score 78.5; DB 5; Length 723;  
 Best Local Similarity 18.0%; Pred. No. 14;  
 RESULT 720  
 ID ADQ97094 standard; protein; 723 AA.  
 DE Human cancer associated sequence Hpl-10-005, SEQ ID 70.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 6.6%; Score 78.5; DB 8; Length 723;  
 Best Local Similarity 18.0%; Pred. No. 14;  
 RESULT 721  
 ID AAB02437 standard; protein; 766 AA.  
 DE Human ATP binding cassette, ABCB9 transporter protein.  
 PN WO200140305-A1.  
 PD 07-JUN-2001.  
 PA (ACT1-) ACTIVE PASS PHARM INC.  
 Query Match 6.6%; Score 78.5; DB 4; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 722  
 ID AAB02441 standard; protein; 766 AA.  
 DE Human ATP binding cassette, ABCB9 transporter protein mutant K545R.  
 PN WO200140305-A1.  
 PD 07-JUN-2001.  
 PA (ACT1-) ACTIVE PASS PHARM INC.  
 Query Match 6.6%; Score 78.5; DB 4; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 723  
 ID AAB02442 standard; protein; 766 AA.  
 DE Human ATP binding cassette, ABCB9 transporter protein mutant D667N.  
 PN WO200140305-A1.  
 PD 07-JUN-2001.  
 PA (ACT1-) ACTIVE PASS PHARM INC.  
 Query Match 6.6%; Score 78.5; DB 4; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 724  
 ID AAG67163 standard; protein; 766 AA.  
 DE Amino acid sequence of a human 33894 transporter polypeptide.  
 PN WO200164875-A2.  
 PD 07-SEP-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 6.6%; Score 78.5; DB 4; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 725  
 ID AAG79246 standard; protein; 766 AA.  
 DE Amino acid sequence of a human TRP-like (HUTAPL) polypeptide.  
 PN WO200173018-A2.  
 PD 04-OCT-2001.  
 PA (MERE-) MERCK PATENT GMBH.  
 Query Match 6.6%; Score 78.5; DB 4; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 726  
 ID ABB98345 standard; protein; 766 AA.  
 DE Human ABC transporter ABCB9 SEQ ID NO 6.  
 PN WO200264781-A2.  
 PD 22-AUG-2002.  
 PA (ACT1-) ACTIVE PASS PHARM INC.  
 Query Match 6.6%; Score 78.5; DB 5; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 727  
 ID AAE21170 standard; protein; 766 AA.  
 DE Human TRICH-14 protein.  
 PN WO200212340-A2.  
 PD 14-FEB-2002.  
 PA (INCY-) INCYTE GENOMICS INC.

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Query Match 6.6%; Score 78.5; DB 5; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 728  
 ID ADQ97096 standard; protein; 766 AA.  
 DE Human cancer associated sequence HP2-10-005, SEQ ID 72.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 6.6%; Score 78.5; DB 8; Length 766;  
 Best Local Similarity 18.0%; Pred. No. 15;  
 RESULT 729  
 ID AAG20805 standard; protein; 377 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23131.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.5%; Score 78; DB 3; Length 377;  
 Best Local Similarity 23.8%; Pred. No. 6.6;  
 RESULT 730  
 ID AAG20804 standard; protein; 442 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23130.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.5%; Score 78; DB 3; Length 442;  
 Best Local Similarity 23.8%; Pred. No. 8.2;  
 RESULT 731  
 ID AAU35545 standard; protein; 471 AA.  
 DE Haemophilus influenzae cellular proliferation protein #186.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 6.5%; Score 78; DB 4; Length 471;  
 Best Local Similarity 25.0%; Pred. No. 9;  
 RESULT 732  
 ID ABU30411 standard; protein; 471 AA.  
 DE Protein encoded by Prokaryotic essential gene #15938.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 6.5%; Score 78; DB 6; Length 471;  
 Best Local Similarity 25.0%; Pred. No. 9;  
 RESULT 733  
 ID AAG20803 standard; protein; 489 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23129.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.5%; Score 78; DB 3; Length 489;  
 Best Local Similarity 23.8%; Pred. No. 9.5;  
 RESULT 734  
 ID ABB49039 standard; protein; 269 AA.  
 DE Listeria monocytogenes protein #1743.  
 PN WO200177335-A2.  
 PD 18-OCT-2001.  
 PA (INSP-) INST PASTEUR.  
 Query Match 6.5%; Score 77.5; DB 5; Length 269;  
 Best Local Similarity 22.0%; Pred. No. 4.7;  
 RESULT 735  
 ID ABE17374 standard; protein; 280 AA.  
 DE Novel human diagnostic protein #17365.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 6.5%; Score 77.5; DB 4; Length 280;  
 Best Local Similarity 21.9%; Pred. No. 5;  
 RESULT 736  
 ID ABO00771 standard; protein; 280 AA.  
 DE Polypeptide encoded by novel human contig #22.  
 PN WO2003023013-A2.  
 PD 20-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 6.5%; Score 77.5; DB 6; Length 280;  
 Best Local Similarity 21.9%; Pred. No. 5;  
 RESULT 737  
 ID ABU4889 standard; protein; 327 AA.

DE Protein encoded by Prokaryotic essential gene #34416.  
 PN W0200277183-A2.  
 PA (ELIT-), ELITRA PHARM INC.  
 Query Match 6.4%; Score 77.5; DB 6; Length 327;  
 Best Local Similarity 24.8%; Pred. No. 6.2;  
 RESULT 738  
 ID AAM13576 standard; protein; 438 AA.  
 DE Mouse Batten disease polypeptide Cln3 homologue.  
 PN W09708308-A1.  
 PD 06-MAR-1997.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (UYLR-) RIJKSUNIV LEIDEN.  
 Query Match 6.5%; Score 77.5; DB 2; Length 436;  
 Best Local Similarity 27.6%; Pred. No. 9.3;  
 RESULT 739  
 ID A0542965 standard; protein; 491 AA.  
 DE Bacterial polypeptide #21395.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 6.5%; Score 77.5; DB 8; Length 491;  
 Best Local Similarity 22.6%; Pred. No. 11;  
 RESULT 740  
 ID ADC42919 standard; protein; 892 AA.  
 DE Variola smallpox virus A10L.  
 PN W02003017943-A2.  
 PD 06-MAR-2003.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 Query Match 6.5%; Score 77.5; DB 7; Length 892;  
 Best Local Similarity 22.7%; Pred. No. 25;  
 RESULT 741  
 ID AAR88413 standard; protein; 353 AA.  
 DE High-affinity melatonin-1a receptor.  
 PN W09535320-A1.  
 PD 28-DEC-1995.  
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 Query Match 6.4%; Score 77; DB 2; Length 353;  
 Best Local Similarity 22.1%; Pred. No. 7.9;  
 RESULT 742  
 ID AAM23958 standard; protein; 353 AA.  
 DE Mouse melatonin 1a receptor.  
 PN W09803549-A1.  
 PD 29-JAN-1998.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 6.4%; Score 77; DB 2; Length 353;  
 Best Local Similarity 22.1%; Pred. No. 7.9;  
 RESULT 743  
 ID ABB07571 standard; protein; 353 AA.  
 DE Mouse melatonin 1a (Me1la) receptor.  
 PN US6326526-B1.  
 PD 04-DEC-2001.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 6.4%; Score 77; DB 5; Length 353;  
 Best Local Similarity 22.1%; Pred. No. 7.9;  
 RESULT 744  
 ID ADO29553 standard; protein; 353 AA.  
 DE Mouse GPCR MTR1A, SEQ ID NO:655.  
 PN W0200404000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIMAL INC.  
 Query Match 6.4%; Score 77; DB 8; Length 353;  
 Best Local Similarity 22.1%; Pred. No. 7.9;  
 RESULT 745  
 ID ADM25403 standard; protein; 383 AA.  
 DE Hyperthermophile Methanopyrus kandleri protein #9.  
 PN W02003076575-A2.  
 PD 18-SEP-2003.

PA (FIDE-) FIDELITY SYSTEMS INC.  
 PA (MALY/) MALYKH A.  
 Query Match 6.4%; Score 77; DB 7; Length 383;  
 Best Local Similarity 24.8%; Pred. No. 8.9;  
 RESULT 746  
 ID ADO95948 standard; protein; 490 AA.  
 DE T cell activation associated protein #63.  
 PN W02004058805-A2.  
 PD 15-JUL-2004.  
 PA (ASAH-) ASAH KASEI PHARMA CORP.  
 Query Match 6.4%; Score 77; DB 8; Length 490;  
 Best Local Similarity 19.5%; Pred. No. 12;  
 RESULT 747  
 ID ADO96002 standard; protein; 490 AA.  
 DE T cell activation associated protein #90.  
 PN W02004058805-A2.  
 PD 15-JUL-2004.  
 PA (ASAH-) ASAH KASEI PHARMA CORP.  
 Query Match 6.4%; Score 77; DB 8; Length 490;  
 Best Local Similarity 19.5%; Pred. No. 12;  
 RESULT 748  
 ID AAG42521 standard; protein; 648 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 53040.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.4%; Score 77; DB 3; Length 648;  
 Best Local Similarity 20.4%; Pred. No. 18;  
 RESULT 749  
 ID ABU16172 standard; protein; 650 AA.  
 DE Protein encoded by Prokaryotic essential gene #1699.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 6.4%; Score 77; DB 6; Length 650;  
 Best Local Similarity 27.5%; Pred. No. 18;  
 RESULT 750  
 ID ABW72713 standard; protein; 650 AA.  
 DE Staphylococcus aureus protein #1953.  
 PN W0200294868-A2.  
 PD 28-NOV-2002.  
 PA (CHIR-) CHIRON SPA.  
 Query Match 6.4%; Score 77; DB 6; Length 650;  
 Best Local Similarity 27.5%; Pred. No. 18;  
 RESULT 751  
 ID AAG42520 standard; protein; 690 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 53039.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.4%; Score 77; DB 3; Length 690;  
 Best Local Similarity 20.4%; Pred. No. 20;  
 RESULT 752  
 ID AAG42519 standard; protein; 728 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 53038.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.4%; Score 77; DB 3; Length 728;  
 Best Local Similarity 20.4%; Pred. No. 22;  
 RESULT 753  
 ID AAG32549 standard; protein; 805 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 39287.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.4%; Score 77; DB 3; Length 805;  
 Best Local Similarity 20.4%; Pred. No. 25;  
 RESULT 754  
 ID AAG32548 standard; protein; 847 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 39286.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.4%; Score 77; DB 3; Length 847;  
 Best Local Similarity 20.4%; Pred. No. 27;  
 RESULT 755  
 ID AAG32547 standard; protein; 991 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 39285.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 20.4%; Score 77; DB 3; Length 991;  
RESULT 756  
ID ABP52133 standard; protein; 1025 AA.  
DE Plasmodium falciparum multidrug resistance protein SEQ ID NO: 85.  
PN EP1217066-A1.  
PD 26-JUN-2002.  
PA (UYGE-) UNIV GENT.  
Query Match  
Best Local Similarity 20.6%; Score 77; DB 5; Length 1025;  
RESULT 757  
ID AAG42381 standard; protein; 1047 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52849.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 20.4%; Score 77; DB 3; Length 1047;  
RESULT 758  
ID AAG42380 standard; protein; 1191 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52848.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 20.4%; Score 77; DB 3; Length 1191;  
RESULT 759  
ID AAG42379 standard; protein; 1202 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52847.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 20.4%; Score 77; DB 3; Length 1202;  
RESULT 760  
ID AAR29527 standard; protein; 2510 AA.  
DE HCV antigen T7N1-30.  
PN EP518313-A2.  
PD 16-DEC-1992.  
PA (MITU) MITSUBISHI KASHI CORP.  
Query Match  
Best Local Similarity 22.5%; Score 77; DB 2; Length 2510;  
RESULT 761  
ID ADF74966 standard; protein; 249 AA.  
DE Human 164-1h protein (SeqID 25).  
PN WO2003097686-A1.  
PD 27-NOV-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 23.3%; Score 76.5; DB 8; Length 249;  
RESULT 762  
ID ADC01137 standard; protein; 278 AA.  
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1181.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match  
Best Local Similarity 28.5%; Score 76.5; DB 7; Length 278;  
RESULT 763  
ID ABO65627 standard; protein; 435 AA.  
DE Klebsiella pneumoniae polypeptide seqid 12344.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 21.8%; Score 76.5; DB 7; Length 435;  
RESULT 764  
ID ADF74969 standard; protein; 481 AA.  
DE Human 164-1b protein (SeqID 28).  
PN WO2003097686-A1.  
PD 27-NOV-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 21.8%; Score 76.5; DB 8; Length 481;

Best Local Similarity 23.3%; Pred. No. 14;  
RESULT 765  
ID AAR90765 standard; protein; 494 AA.  
DE Human K+ channel 2 mature protein.  
PN WO9603415-A1.  
PD 08-FEB-1996.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 21.3%; Score 76.5; DB 2; Length 494;  
RESULT 766  
ID AAM42996 standard; protein; 494 AA.  
DE Putative mature potassium channel 2 protein.  
PN US5710019-A.  
PD 20-JAN-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 21.3%; Score 76.5; DB 2; Length 494;  
RESULT 767  
ID ABP58356 standard; protein; 494 AA.  
DE Human potassium channel subunit Kv5.1.  
PN WO200296944-A2.  
PD 05-DEC-2002.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Query Match  
Best Local Similarity 21.3%; Score 76.5; DB 6; Length 494;  
RESULT 768  
ID ADC99155 standard; protein; 494 AA.  
DE Human mature K+ channel 2 protein.  
PN US2003092895-A1.  
PD 15-MAY-2003.  
PA (LITY/) LI Y.  
PA (ADAM/) ADAMS M D.  
PA (WHIT/) WHITE O R.  
Query Match  
Best Local Similarity 21.3%; Score 76.5; DB 7; Length 494;  
RESULT 769  
ID AAW20085 standard; protein; 509 AA.  
DE Helicobacter pylori cytoplasmic protein, 10009666.a.  
PN WO9640893-A1.  
PD 19-DEC-1996.  
PA (ASTR-) ASTRA AB.  
Query Match  
Best Local Similarity 19.2%; Score 76.5; DB 2; Length 509;  
RESULT 770  
ID ADQ07984 standard; protein; 526 AA.  
DE Human hypothetical protein FLJ20371-encoding cDNA.  
PN WO2004061123-A2.  
PD 22-JUL-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 15.7%; Score 76.5; DB 8; Length 526;  
RESULT 771  
ID ADP25065 standard; protein; 526 AA.  
DE PRO polypeptide SEQ ID NO: 2243.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GENT-) GENENTECH INC.  
Query Match  
Best Local Similarity 15.7%; Score 76.5; DB 8; Length 526;  
RESULT 772  
ID ADB63857 standard; protein; 555 AA.  
DE Human protein encoded by clone ASTRO20053430.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELT-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 23.3%; Score 76.5; DB 7; Length 555;  
RESULT 773  
ID ABB08159 standard; protein; 570 AA.  
DE Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).  
PN WO200242330-A2.  
PD 30-MAY-2002.

PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 6.4%; Score 76.5; DB 5; Length 570;  
 Best Local Similarity 23.3%; Pred. No. 18;  
 RESULT 774  
 ID AAM20918 standard; protein; 593 AA.  
 DE H. pylori transporter protein, 149p12015orf14.  
 PN M09640893-A1.  
 PD 19-DEC-1996.  
 PA (ASTR) ASTRA AB.  
 Query Match 6.4%; Score 76.5; DB 2; Length 593;  
 Best Local Similarity 19.2%; Pred. No. 19;  
 RESULT 775  
 ID ADN46225 standard; protein; 615 AA.  
 DE Thermococcus kodakaraensis KOD1 protein sequence SeqID103.  
 PN M02004022735-A1.  
 PD 18-MAR-2004.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Query Match 6.4%; Score 76.5; DB 8; Length 615;  
 Best Local Similarity 22.6%; Pred. No. 20;  
 RESULT 776  
 ID ADN21126 standard; protein; 2539 AA.  
 DE Bacterial polypeptide #3779.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 6.4%; Score 76.5; DB 8; Length 2539;  
 Best Local Similarity 22.1%; Pred. No. 1.4e+02;  
 RESULT 777  
 ID ADH88107 standard; protein; 195 AA.  
 DE Enterococcus faecalis polypeptide #2587.  
 PN US6617156-B1.  
 PD 09-SEP-2003.  
 PA (DOUC/) DOUCETTE-STAMM L A.  
 PA (BUSH/) BUSH D.  
 Query Match 6.4%; Score 76; DB 7; Length 195;  
 Best Local Similarity 25.9%; Pred. No. 4.6;  
 RESULT 778  
 ID AAG09592 standard; protein; 274 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 7585.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.4%; Score 76; DB 3; Length 274;  
 Best Local Similarity 26.7%; Pred. No. 7.3;  
 RESULT 779  
 ID AAG09591 standard; protein; 287 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 7585.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.4%; Score 76; DB 3; Length 287;  
 Best Local Similarity 26.7%; Pred. No. 7.8;  
 RESULT 780  
 ID ADQ96244 standard; protein; 366 AA.  
 DE T cell activation associated protein #211.  
 PN M02004058805-A2.  
 PD 15-JUL-2004.  
 PA (ASAH-) ASAH KASEI PHARMA CORP.  
 Query Match 6.4%; Score 76; DB 8; Length 366;  
 Best Local Similarity 22.0%; Pred. No. 11;  
 RESULT 781  
 ID ADQ96246 standard; protein; 366 AA.  
 DE T cell activation associated protein #212.  
 PN M02004058805-A2.  
 PD 15-JUL-2004.  
 PA (ASAH-) ASAH KASEI PHARMA CORP.  
 Query Match 6.4%; Score 76; DB 8; Length 366;  
 Best Local Similarity 22.0%; Pred. No. 11;  
 RESULT 782  
 ID ABB89424 standard; protein; 456 AA.  
 DE Human polypeptide SEQ ID NO 1800.

PN M0200190304-A2.  
 PD 28-NOV-2001.  
 PA (HUMA-) HUMA GENOME SCI INC.  
 Query Match 6.4%; Score 76; DB 5; Length 456;  
 Best Local Similarity 22.0%; Pred. No. 15;  
 RESULT 783  
 ID AAB53400 standard; protein; 557 AA.  
 DE Human colon cancer antigen protein sequence SEQ ID NO:940.  
 PN M0200055351-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMA GENOME SCI INC.  
 Query Match 6.4%; Score 76; DB 3; Length 557;  
 Best Local Similarity 22.0%; Pred. No. 20;  
 RESULT 784  
 ID AAY44945 standard; protein; 593 AA.  
 DE Mneat sulphate permease-2.  
 PN M0200004154-A2.  
 PD 27-JAN-2000.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 Query Match 6.4%; Score 76; DB 3; Length 593;  
 Best Local Similarity 21.4%; Pred. No. 21;  
 RESULT 785  
 ID ADN22849 standard; protein; 1402 AA.  
 DE Bacterial polypeptide #5502.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 6.4%; Score 76; DB 8; Length 1402;  
 Best Local Similarity 20.2%; Pred. No. 70;  
 RESULT 786  
 ID ADN23383 standard; protein; 1917 AA.  
 DE Bacterial polypeptide #6036.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 6.4%; Score 76; DB 8; Length 1917;  
 Best Local Similarity 18.5%; Pred. No. 1.1e+02;  
 RESULT 787  
 ID AAB63150 standard; protein; 228 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 16242.  
 PN M0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 6.3%; Score 75.5; DB 4; Length 228;  
 Best Local Similarity 21.8%; Pred. No. 6.5;  
 RESULT 788  
 ID ADK46633 standard; protein; 263 AA.  
 DE Streptococcus pneumoniae protein, Seq ID No 3148.  
 PN US6699703-B1.  
 PD 02-MAR-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 6.3%; Score 75.5; DB 8; Length 263;  
 Best Local Similarity 18.0%; Pred. No. 7.9;  
 RESULT 789  
 ID ADM92206 standard; protein; 263 AA.  
 DE S pneumoniae antigenic protein sequence SeqID403.  
 PN M02004020609-A2.  
 PD 11-MAR-2004.  
 PA (TUFT) UNIV TUFTS.  
 Query Match 6.3%; Score 75.5; DB 8; Length 263;  
 Best Local Similarity 18.0%; Pred. No. 7.9;  
 RESULT 790  
 ID AAY81619 standard; protein; 264 AA.  
 DE Streptococcus pneumoniae type 4 protein sequence #119.  
 PN M0200006737-A2.

PD 10-FEB-2000.  
PA (MICR-) MICROBIAL TECHNICS LTD.  
Query Match 6.3%; Score 75.5; DB 3; Length 264;  
Best Local Similarity 18.0%; Pred. No. 7.9;  
RESULT 791  
ID ADR96242 standard; protein; 264 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 4877.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.3%; Score 75.5; DB 8; Length 264;  
Best Local Similarity 18.0%; Pred. No. 7.9;  
RESULT 792  
ID AEU02182 standard; protein; 276 AA.  
DE S. pneumoniae type 4 strain protein from coding region #1759.  
PN W0200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.3%; Score 75.5; DB 6; Length 276;  
Best Local Similarity 18.0%; Pred. No. 8.4;  
RESULT 793  
ID AAG93285 standard; protein; 342 AA.  
DE C. albicans BAX-associated protein fragment SEQ ID 528.  
PN W0200264766-A2.  
PD 22-AUG-2002.  
PA (JANC) JANSSEN PHARM NV.  
Query Match 6.3%; Score 75.5; DB 5; Length 342;  
Best Local Similarity 21.9%; Pred. No. 11;  
RESULT 794  
ID AAB15936 standard; protein; 352 AA.  
DE E. coli proliferation associated protein sequence SEQ ID NO:293.  
PN W0200044906-A2.  
PD 03-AUG-2000.  
PA (BLIT-) BLITRA PHARM INC.  
Query Match 6.3%; Score 75.5; DB 3; Length 352;  
Best Local Similarity 31.7%; Pred. No. 12;  
RESULT 795  
ID ADH51470 standard; protein; 363 AA.  
DE Rat M1 receptor amino acid sequence #SEQ ID 2.  
PN PR2835847-A1.  
PD 15-AUG-2003.  
PA (SERV-) LES LAB SERVIER SA.  
Query Match 6.3%; Score 75.5; DB 7; Length 363;  
Best Local Similarity 23.5%; Pred. No. 12;  
RESULT 796  
ID AAU03851 standard; protein; 397 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.  
PN W0200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA) PHARMACIA & UPJOHN.  
Query Match 6.3%; Score 75.5; DB 4; Length 397;  
Best Local Similarity 19.1%; Pred. No. 14;  
RESULT 797  
ID AAU03852 standard; protein; 433 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.  
PN W0200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA) PHARMACIA & UPJOHN.  
Query Match 6.3%; Score 75.5; DB 4; Length 433;  
Best Local Similarity 19.1%; Pred. No. 16;  
RESULT 798  
ID ADS24239 standard; protein; 463 AA.  
DE Bacterial polypeptide #13722.  
PN US200233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 6.3%; Score 75.5; DB 8; Length 463;  
Best Local Similarity 21.4%; Pred. No. 17;  
RESULT 799  
ID ADO29507 standard; protein; 471 AA.  
DE Mouse GPCR HTR2A, SEQ ID NO:609.  
PN W0200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMM INC.  
Query Match 6.3%; Score 75.5; DB 8; Length 471;  
Best Local Similarity 21.0%; Pred. No. 18;  
RESULT 800  
ID AAU03820 standard; protein; 499 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.  
PN W0200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA) PHARMACIA & UPJOHN.  
Query Match 6.3%; Score 75.5; DB 4; Length 499;  
Best Local Similarity 19.1%; Pred. No. 19;  
RESULT 801  
ID ADM72132 standard; protein; 392 AA.  
DE Human NTRAN polypeptide (clone ID 752455CD1).  
PN W02004022705-A2.  
PD 18-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.3%; Score 75; DB 8; Length 392;  
Best Local Similarity 21.0%; Pred. No. 16;  
RESULT 802  
ID AAU45917 standard; protein; 445 AA.  
DE Propionibacterium acnes immunogenic protein #6813.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 6.3%; Score 75; DB 4; Length 445;  
Best Local Similarity 24.8%; Pred. No. 19;  
RESULT 803  
ID AAM42436 standard; protein; 445 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7112.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 6.3%; Score 75; DB 6; Length 445;  
Best Local Similarity 24.8%; Pred. No. 19;  
RESULT 804  
ID ADA34178 standard; protein; 467 AA.  
DE Actinobacter Daumann1 protein #1339.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.3%; Score 75; DB 6; Length 467;  
Best Local Similarity 23.1%; Pred. No. 20;  
RESULT 805  
ID ADR14597 standard; protein; 473 AA.  
DE Human NF-kappaB pathway-associated protein SeqID598.  
PN W02004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.3%; Score 75; DB 8; Length 473;  
Best Local Similarity 21.0%; Pred. No. 20;  
RESULT 806  
ID ADP99138 standard; protein; 480 AA.  
DE Human transporter and ion channel (TRICH) protein - SEQ ID 3.  
PN W02004048599-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.3%; Score 75; DB 8; Length 480;  
Best Local Similarity 21.0%; Pred. No. 21;  
RESULT 807  
ID ADH86490 standard; protein; 549 AA.  
DE Enterococcus faecalis polypeptide #970.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC) DOUCETTE-STAMM L A.  
PA (BUSH) BUSH D.  
Query Match 6.3%; Score 75; DB 7; Length 549;  
Best Local Similarity 18.7%; Pred. No. 25;



RESULT 808  
ID AAB54066 standard; protein; 1051 AA.  
DE Non-A, non-B hepatitis virus gene #4 product.  
PN JP06141870-A.  
PD 24-MAY-1994.  
PA (TOKR-) ZH TOKYO IGAKU SOGO KENKYUSHO.  
PA (SANN) SANWA KAGAKU KENKYUSHO CO.  
PA (TOFU) TONEN CORP.  
Query Match 6.3%; Score 75; DB 2; Length 1051;  
Best Local Similarity 23.4%; Pred. No. 62;  
RESULT 809  
ID AAR98361 standard; protein; 1051 AA.  
DE 5-UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).  
PN JP07133291-A.  
PD 23-MAY-1995.  
PA (TOFU) TONEN CORP.  
Query Match 6.3%; Score 75; DB 2; Length 1051;  
Best Local Similarity 23.4%; Pred. No. 62;  
RESULT 810  
ID ADB64712 standard; protein; 1131 AA.  
DE Human protein encoded by clone NT2NE20077270.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.3%; Score 75; DB 7; Length 1131;  
Best Local Similarity 23.9%; Pred. No. 68;  
RESULT 811  
ID AAB64494 standard; protein; 2248 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 20274.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.3%; Score 75; DB 4; Length 2248;  
Best Local Similarity 22.9%; Pred. No. 1.8e+02;  
RESULT 812  
ID ADG20763 standard; protein; 2248 AA.  
DE Drosophila melanogaster rutabaga protein SEQ ID NO:2.  
PN WO2003103704-A2.  
PD 18-DEC-2003.  
PA (DEVE-) DEVELOPMENTAL BIOLOGISCHE FORSCH.  
Query Match 6.3%; Score 75; DB 8; Length 2248;  
Best Local Similarity 22.9%; Pred. No. 1.8e+02;  
RESULT 813  
ID ADQ89856 standard; protein; 2248 AA.  
DE Antagonist of cell cycle progression polypeptide #43.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 6.3%; Score 75; DB 8; Length 2248;  
Best Local Similarity 22.9%; Pred. No. 1.8e+02;  
RESULT 814  
ID AAB66797 standard; protein; 200 AA.  
DE Porcine reproductive and respiratory syndrome virus ORF #5 protein.  
PN WO200102858-A1.  
PD 11-JAN-2001.  
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.  
PA (MATE-) INST MATERIALS RES & ENG.  
Query Match 6.2%; Score 74.5; DB 4; Length 200;  
Best Local Similarity 23.8%; Pred. No. 7.1;  
RESULT 815  
ID ADP74954 standard; protein; 256 AA.  
DE Rat 164-1h protein (SeqID 13).  
PN WO2003097686-A1.  
PD 27-NOV-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 6.2%; Score 74.5; DB 8; Length 256;  
Best Local Similarity 23.3%; Pred. No. 10;  
RESULT 816  
ID AAR53748 standard; protein; 355 AA.  
DE Seven transmembrane receptor (V28).  
PN WO9412635-A2.  
PD 09-JUN-1994.

PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 2; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 817  
ID AAW48722 standard; protein; 355 AA.  
DE Human V28 seven transmembrane receptor.  
PN US5759804-A.  
PD 02-JUN-1998.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 2; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 818  
ID AAY90677 standard; protein; 355 AA.  
DE Human mutant G protein-coupled receptor V28 (I230K).  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 819  
ID AAY90642 standard; protein; 355 AA.  
DE Human G protein-coupled receptor V28.  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 820  
ID AAB21693 standard; protein; 355 AA.  
DE Human 7TM receptor V28 cDNA clone protein #2.  
PN US6107475-A.  
PD 22-AUG-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 821  
ID AAB21692 standard; protein; 355 AA.  
DE Human 7TM receptor V28 cDNA clone protein #1.  
PN US6107475-A.  
PD 22-AUG-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 822  
ID AAG80126 standard; protein; 355 AA.  
DE Human CX3CR1 protein.  
PN WO200172830-A2.  
PD 04-OCT-2001.  
PA (IFP-) IPF PHARM GMBH.  
PA (FORS-) FORSMANN U.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 823  
ID AAB82786 standard; protein; 355 AA.  
DE Human CX3C chemokine receptor 1.  
PN WO200160406-A1.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
PA (NOUN) UNIV NORTHWESTERN.  
Query Match 6.2%; Score 74.5; DB 4; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 824  
ID AAU91235 standard; protein; 355 AA.  
DE Human 7 transmembrane domain receptor V28 #2.  
PN US6348574-B1.  
PD 19-FEB-2002.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 5; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 825  
ID AAU91234 standard; protein; 355 AA.  
DE Human 7 transmembrane domain receptor V28 #1.  
PN US6348574-B1.

PD 19-FEB-2002.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 5; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 826  
ID AAU84327 standard; protein; 355 AA.  
DE Protein CX3CR1 differentially expressed in breast cancer tissue.  
PN WO200210436-A2.  
PD 07-FEB-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
PA (BAAK/) BAAK J.  
Query Match 6.2%; Score 74.5; DB 5; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 827  
ID ABR58524 standard; protein; 355 AA.  
DE Human chemokine (C-X3-C) receptor 1 protein.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (BOSB-) BOS BIOTECHNOLOGY INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 828  
ID AAO29513 standard; protein; 355 AA.  
DE Human fractalkine receptor (313) protein.  
PN WO2003039475-A2.  
PD 15-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 829  
ID ABP97732 standard; protein; 355 AA.  
DE Amino acid sequence of human chemokine receptor CX3CR1.  
PN WO2003014153-A2.  
PD 20-FEB-2003.  
PA (TOP1-) TOPIGEN PHARM INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 830  
ID ABP81882 standard; protein; 355 AA.  
DE Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 831  
ID ADC22751 standard; protein; 355 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #74.  
PN US655339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 832  
ID ADC22649 standard; protein; 355 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #34.  
PN US655339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 833  
ID ADH14224 standard; protein; 355 AA.  
DE Mutated human serotonin V28.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 834  
ID ADH14122 standard; protein; 355 AA.

DE Human serotonin V28.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 835  
ID ADH10680 standard; protein; 355 AA.  
DE Human CX3CR1 polypeptide.  
PN WO2003104484-A1.  
PD 18-DEC-2003.  
PA (META-) METABOLEX INC.  
Query Match 6.2%; Score 74.5; DB 8; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 836  
ID ADO29269 standard; protein; 355 AA.  
DE Human GPCR CX3CR1, SEQ ID NO:370.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMML INC.  
Query Match 6.2%; Score 74.5; DB 8; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 837  
ID ADQ18141 standard; protein; 355 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 958.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.2%; Score 74.5; DB 8; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 838  
ID ADP56020 standard; protein; 355 AA.  
DE Human PRO protein sequence SEQ ID NO:1996.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 6.2%; Score 74.5; DB 8; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 839  
ID ADP54585 standard; protein; 355 AA.  
DE Human PRO protein sequence SEQ ID NO:561.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 6.2%; Score 74.5; DB 8; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 840  
ID ADP23931 standard; protein; 355 AA.  
DE PRO polypeptide SEQ ID NO:1109.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 6.2%; Score 74.5; DB 8; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 841  
ID ADO39421 standard; protein; 355 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1084.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.2%; Score 74.5; DB 8; Length 355;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 842  
ID ADO39422 standard; protein; 362 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1085.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.2%; Score 74.5; DB 8; Length 362;  
Best Local Similarity 25.8%; Pred. No. 16;  
RESULT 843

ID AAM7109 standard; protein; 471 AA.  
DE Rat 5-HT2A serotonin receptor C322K mutant.  
PN WO9838217-A1.  
PD 03-SEP-1998.  
PA (TEIT/) TEITLER M.  
PA (HERR/) HERRICK-DAVIS K.  
PA (EGAN/) EGAN C C.  
Query Match 6.2%; Score 74.5; DB 2; Length 471;  
Best Local Similarity 21.0%; Pred. No. 23;  
RESULT 844  
ID AAM7111 standard; protein; 471 AA.  
DE Rat 5-HT2A serotonin receptor C322E mutant.  
PN WO9838217-A1.  
PD 03-SEP-1998.  
PA (TEIT/) TEITLER M.  
PA (HERR/) HERRICK-DAVIS K.  
PA (EGAN/) EGAN C C.  
Query Match 6.2%; Score 74.5; DB 2; Length 471;  
Best Local Similarity 21.0%; Pred. No. 23;  
RESULT 845  
ID AAM7110 standard; protein; 471 AA.  
DE Rat 5-HT2A serotonin receptor C322R mutant.  
PN WO9838217-A1.  
PD 03-SEP-1998.  
PA (TEIT/) TEITLER M.  
PA (HERR/) HERRICK-DAVIS K.  
PA (EGAN/) EGAN C C.  
Query Match 6.2%; Score 74.5; DB 2; Length 471;  
Best Local Similarity 21.0%; Pred. No. 23;  
RESULT 846  
ID AAM7104 standard; protein; 471 AA.  
DE Rat 5-HT2A serotonin receptor.  
PN WO9838217-A1.  
PD 03-SEP-1998.  
PA (TEIT/) TEITLER M.  
PA (HERR/) HERRICK-DAVIS K.  
PA (EGAN/) EGAN C C.  
Query Match 6.2%; Score 74.5; DB 2; Length 471;  
Best Local Similarity 21.0%; Pred. No. 23;  
RESULT 847  
ID AAB07980 standard; protein; 471 AA.  
DE Rat 5-HT2 receptor sequence.  
PN US6383762-B1.  
PD 07-MAY-2002.  
PA (SYNA-) SYNAPTC PHARM CORP.  
Query Match 6.2%; Score 74.5; DB 5; Length 471;  
Best Local Similarity 21.0%; Pred. No. 23;  
RESULT 848  
ID ADF74971 standard; protein; 481 AA.  
DE Rat 164-1b protein (SeqID 30).  
PN WO2003097686-A1.  
PD 27-NOV-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 6.2%; Score 74.5; DB 8; Length 481;  
Best Local Similarity 23.3%; Pred. No. 24;  
RESULT 849  
ID AAM93692 standard; protein; 562 AA.  
DE Human polypeptide, SEQ ID NO: 3602.  
PN EP130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 6.2%; Score 74.5; DB 4; Length 562;  
Best Local Similarity 23.1%; Pred. No. 30;  
RESULT 850  
ID ADL31569 standard; protein; 562 AA.  
DE Human protein encoded by a full length CDNA clone SeqID 3602.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.2%; Score 74.5; DB 8; Length 562;  
Best Local Similarity 23.1%; Pred. No. 30;  
RESULT 851  
ID ADQ96138 standard; protein; 562 AA.

DE T cell activation associated protein #158.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 6.2%; Score 74.5; DB 8; Length 562;  
Best Local Similarity 23.1%; Pred. No. 30;  
RESULT 852  
ID ADR86160 standard; protein; 587 AA.  
DE Aspergillus fumigatus essential gene protein #210.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match 6.2%; Score 74.5; DB 8; Length 587;  
Best Local Similarity 18.2%; Pred. No. 32;  
RESULT 853  
ID ABB62948 standard; protein; 597 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15636.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.2%; Score 74.5; DB 4; Length 597;  
Best Local Similarity 27.2%; Pred. No. 32;  
RESULT 854  
ID ADA36878 standard; protein; 940 AA.  
DE Acinetobacter baumannii protein #4039.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 74.5; DB 6; Length 940;  
Best Local Similarity 21.1%; Pred. No. 61;  
RESULT 855  
ID ABB92731 standard; protein; 1808 AA.  
DE Herbicidally active polypeptide SEQ ID NO 1942.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 6.2%; Score 74.5; DB 5; Length 1808;  
Best Local Similarity 17.3%; Pred. No. 1.5e+02;  
RESULT 856  
ID AAE20477 standard; protein; 3010 AA.  
DE HCV-S1 full-length polypeptide.  
PN WO200208447-A2.  
PD 31-JAN-2002.  
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
PA (EHRU-) EHRUCH G.  
Query Match 6.2%; Score 74.5; DB 5; Length 3010;  
Best Local Similarity 23.8%; Pred. No. 3e+02;  
RESULT 857  
ID ADF07294 standard; protein; 154 AA.  
DE Bacterial polypeptide #3407.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 74; DB 7; Length 154;  
Best Local Similarity 26.4%; Pred. No. 5.6;  
RESULT 858  
ID ABO70365 standard; protein; 231 AA.  
DE Human adipocyte balt protein, melatonin receptor\_V4.  
PN WO200286122-A2.  
PD 31-OCT-2002.  
PA (HYBR-) HYBRIGENICS.  
Query Match 6.2%; Score 74; DB 6; Length 231;  
Best Local Similarity 18.5%; Pred. No. 9.9;  
RESULT 859  
ID ABO70366 standard; protein; 231 AA.  
DE Human adipocyte balt protein, melatonin receptor\_V5.  
PN WO200286122-A2.  
PD 31-OCT-2002.  
PA (HYBR-) HYBRIGENICS.  
Query Match 6.2%; Score 74; DB 6; Length 231;  
Best Local Similarity 18.5%; Pred. No. 9.9;  
RESULT 860

ID ABB54180 standard; protein; 312 AA.  
DE Lactococcus lactis protein y1lg.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.2%; Score 74; DB 5; Length 312;  
Best Local Similarity 24.3%; Pred. No. 15;  
RESULT 861  
ID ADS44483 standard; protein; 312 AA.  
DE Bacterial polypeptide #22913.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY ) CAO Y.  
PA (HINK ) HINKLE G J.  
PA (SLAT ) SLATER S C.  
PA (CHEN ) CHEN X.  
PA (GOLD ) GOLDMAN B S.  
Query Match 6.2%; Score 74; DB 8; Length 312;  
Best Local Similarity 38.3%; Pred. No. 15;  
RESULT 862  
ID ABB02869 standard; protein; 324 AA.  
DE S. pneumoniae type 4 strain protein from coding region #2450.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR ) CHIRON SPA.  
PA (GENO ) INST GENOMIC RES.  
Query Match 6.2%; Score 74; DB 6; Length 324;  
Best Local Similarity 24.3%; Pred. No. 16;  
RESULT 863  
ID ABR94027 standard; protein; 332 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 2662.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO ) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 74; DB 8; Length 332;  
Best Local Similarity 24.3%; Pred. No. 16;  
RESULT 864  
ID ABO00448 standard; protein; 342 AA.  
DE Novel human polypeptide #35.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE ) HYSEQ INC.  
Query Match 6.2%; Score 74; DB 6; Length 342;  
Best Local Similarity 21.2%; Pred. No. 17;  
RESULT 865  
ID AAR88412 standard; protein; 350 AA.  
DE High-affinity melatonin-1a receptor.  
PN WO9535320-A1.  
PD 28-DEC-1995.  
PA (MASS ) MASSACHUSETTS GEN HOSPITAL.  
Query Match 6.2%; Score 74; DB 2; Length 350;  
Best Local Similarity 18.5%; Pred. No. 18;  
RESULT 866  
ID AAM15786 standard; protein; 350 AA.  
DE Melatonin receptor protein.  
PN JP09084581-A.  
PD 31-MAR-1997.  
PA (TAKA ) TAKEDA CHEM IND LTD.  
Query Match 6.2%; Score 74; DB 2; Length 350;  
Best Local Similarity 18.5%; Pred. No. 18;  
RESULT 867  
ID AAM94761 standard; protein; 350 AA.  
DE Human melatonin receptor protein mel-1a.  
PN EP892046-A2.  
PD 20-JAN-1999.  
PA (JCRP ) JCR PHARM CO LTD.  
Query Match 6.2%; Score 74; DB 2; Length 350;  
Best Local Similarity 18.5%; Pred. No. 18;  
RESULT 868  
ID ABB81840 standard; protein; 350 AA.  
DE Human melatonin receptor type 1a protein SEQ ID NO:164.  
PN WO200261087-A2.  
PD 08-AUG-2002.

PA (LIFE ) LIFESPAN BIOSCIENCES INC.  
Query Match 6.2%; Score 74; DB 6; Length 350;  
Best Local Similarity 18.5%; Pred. No. 18;  
RESULT 869  
ID ADO29552 standard; protein; 350 AA.  
DE Human GPCR MTNRIA, SEQ ID NO:654.  
PN WO200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM ) PRIMAL INC.  
Query Match 6.2%; Score 74; DB 8; Length 350;  
Best Local Similarity 18.5%; Pred. No. 18;  
RESULT 870  
ID AAM19220 standard; protein; 364 AA.  
DE Rat growth hormone secretagogue receptor type Ia.  
PN WO9721730-A1.  
PD 19-JUN-1997.  
PA (MERI ) MERCK & CO INC.  
Query Match 6.2%; Score 74; DB 2; Length 364;  
Best Local Similarity 19.4%; Pred. No. 19;  
RESULT 871  
ID AAM73179 standard; protein; 366 AA.  
DE Staphylococcus aureus protein #2419.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR ) CHIRON SPA.  
Query Match 6.2%; Score 74; DB 6; Length 366;  
Best Local Similarity 21.8%; Pred. No. 19;  
RESULT 872  
ID ABB55224 standard; protein; 442 AA.  
DE Lactococcus lactis protein yred.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.2%; Score 74; DB 5; Length 442;  
Best Local Similarity 20.4%; Pred. No. 24;  
RESULT 873  
ID ADN23927 standard; protein; 485 AA.  
DE Bacterial polypeptide #6580.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY ) CAO Y.  
PA (HINK ) HINKLE G J.  
PA (SLAT ) SLATER S C.  
PA (CHEN ) CHEN X.  
PA (GOLD ) GOLDMAN B S.  
Query Match 6.2%; Score 74; DB 8; Length 485;  
Best Local Similarity 26.2%; Pred. No. 28;  
RESULT 874  
ID AAY80509 standard; protein; 492 AA.  
DE F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.  
PN WO200008170-A1.  
PD 17-FEB-2000.  
PA (SAOC ) MERCIAN CORP.  
Query Match 6.2%; Score 74; DB 3; Length 492;  
Best Local Similarity 22.5%; Pred. No. 28;  
RESULT 875  
ID AAG64105 standard; protein; 493 AA.  
DE Flavobacterium lutescens L-lysine-6-aminotransferase.  
PN WO200148216-A1.  
PD 05-JUL-2001.  
PA (SAOC ) MERCIAN CORP.  
Query Match 6.2%; Score 74; DB 4; Length 493;  
Best Local Similarity 22.5%; Pred. No. 28;  
RESULT 876  
ID AAR54067 standard; protein; 1031 AA.  
DE Non-A, non-B hepatitis virus gene #6 product.  
PN JP06141870-A.  
PD 24-MAY-1994.  
PA (TOKR ) ZH TOKYO TO KINSHO IGAKU SOGO KENKYUSHO.  
PA (SANW ) SANWA KAGAKU KENKYUSHO CO.  
PA (TOFU ) TONEN CORP.  
Query Match 6.2%; Score 74; DB 2; Length 1031;  
Best Local Similarity 26.2%; Pred. No. 79;

RESULT 877  
ID AAR98362 standard; protein; 1031 AA.  
DE 5' UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).  
PN JP07133291-A.  
PD 23-MAY-1995.  
PA (TOFU) TONEN CORP.  
Query Match 6.2%; Score 74; DB 2; Length 1031;  
Best Local Similarity 26.2%; Pred. No. 79;  
RESULT 878  
ID AAG59839 standard; protein; 120 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 73.5; DB 3; Length 120;  
Best Local Similarity 20.3%; Pred. No. 4.6;  
RESULT 879  
ID AAU5578 standard; protein; 192 AA.  
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.  
PN W0200162797-A2.  
PD 30-AUG-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 6.2%; Score 73.5; DB 4; Length 192;  
Best Local Similarity 26.3%; Pred. No. 8.8;  
RESULT 880  
ID ABU4404 standard; protein; 268 AA.  
DE Protein encoded by Prokaryotic essential gene #29571.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.2%; Score 73.5; DB 6; Length 268;  
Best Local Similarity 19.6%; Pred. No. 14;  
RESULT 881  
ID AAG3248 standard; protein; 282 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 73.5; DB 3; Length 282;  
Best Local Similarity 28.1%; Pred. No. 15;  
RESULT 882  
ID ADF05982 standard; protein; 312 AA.  
DE Bacterial polypeptide #2095.  
PN U6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 73.5; DB 7; Length 312;  
Best Local Similarity 17.4%; Pred. No. 17;  
RESULT 883  
ID AAG51386 standard; protein; 377 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65212.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 73.5; DB 3; Length 377;  
Best Local Similarity 28.1%; Pred. No. 22;  
RESULT 884  
ID AAG32487 standard; protein; 377 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39199.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 73.5; DB 3; Length 377;  
Best Local Similarity 28.1%; Pred. No. 22;  
RESULT 885  
ID AD075734 standard; protein; 404 AA.  
DE Codon optimised hCMV IE1 encoded exons 2 and 4.  
PN W02004058166-A2.  
PD 15-JUL-2004.  
PA (VIC-) VICAL INC.  
Query Match 6.2%; Score 73.5; DB 8; Length 404;  
Best Local Similarity 19.3%; Pred. No. 25;  
RESULT 886  
ID AAG5185 standard; protein; 442 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65211.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 73.5; DB 3; Length 442;  
Best Local Similarity 28.1%; Pred. No. 28;  
RESULT 887  
ID AAG32486 standard; protein; 442 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39198.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 73.5; DB 3; Length 442;  
Best Local Similarity 28.1%; Pred. No. 28;  
RESULT 888  
ID AAG5184 standard; protein; 489 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65210.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 73.5; DB 3; Length 489;  
Best Local Similarity 28.1%; Pred. No. 32;  
RESULT 889  
ID AAB86544 standard; protein; 491 AA.  
DE Human cytomegalovirus strain AD169 IE1 protein.  
PN W0200163386-A2.  
PD 30-AUG-2001.  
PA (KERN-) KERN F.  
Query Match 6.2%; Score 73.5; DB 4; Length 491;  
Best Local Similarity 19.3%; Pred. No. 32;  
RESULT 890  
ID ADP12517 standard; protein; 491 AA.  
DE Protein encoded by mRNA of the invention #127.  
PN W02004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 6.2%; Score 73.5; DB 8; Length 491;  
Best Local Similarity 19.3%; Pred. No. 32;  
RESULT 891  
ID ADP12518 standard; protein; 491 AA.  
DE Protein encoded by mRNA of the invention #128.  
PN W02004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 6.2%; Score 73.5; DB 8; Length 491;  
Best Local Similarity 19.3%; Pred. No. 32;  
RESULT 892  
ID ADP12513 standard; protein; 491 AA.  
DE Protein encoded by mRNA of the invention #123.  
PN W02004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 6.2%; Score 73.5; DB 8; Length 491;  
Best Local Similarity 19.3%; Pred. No. 32;  
RESULT 893  
ID ADP12514 standard; protein; 491 AA.  
DE Protein encoded by mRNA of the invention #124.  
PN W02004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 6.2%; Score 73.5; DB 8; Length 491;  
Best Local Similarity 19.3%; Pred. No. 32;  
RESULT 894  
ID ADG75725 standard; protein; 491 AA.  
DE Wild type hCMV IE1.  
PN W02004058166-A2.  
PD 15-JUL-2004.  
PA (VIC-) VICAL INC.  
Query Match 6.2%; Score 73.5; DB 8; Length 491;  
Best Local Similarity 19.3%; Pred. No. 32;  
RESULT 895  
ID ABP73574 standard; protein; 574 AA.  
DE Candida albicans essential protein SEQ ID NO 7411.  
PN W0200253728-A2.  
PD 11-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.2%; Score 73.5; DB 5; Length 574;  
Best Local Similarity 20.8%; Pred. No. 40;  
RESULT 896

ID AD528278 standard; protein; 637 AA.  
DE Bacterial polypeptide #17311.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.2%; Score 73.5; DB 8; Length 637;  
Best Local Similarity 28.3%; Pred. No. 46;  
RESULT 897  
ID ABG29128 standard; protein; 682 AA.  
DE Novel human diagnostic protein #29119.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.2%; Score 73.5; DB 4; Length 682;  
Best Local Similarity 20.0%; Pred. No. 51;  
RESULT 898  
ID ABB61737 standard; protein; 1287 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12003.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE/) PE CORP NY.  
Query Match 6.2%; Score 73.5; DB 4; Length 1287;  
Best Local Similarity 18.2%; Pred. No. 1.2e+02;  
RESULT 899  
ID ADS96670 standard; protein; 1287 AA.  
DE Drosophila melanogaster protein, SEQ ID 291.  
PN WO200403999-A2.  
PD 13-MAY-2004.  
PA (SYGN/) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.2%; Score 73.5; DB 8; Length 1287;  
Best Local Similarity 18.2%; Pred. No. 1.2e+02;  
RESULT 900  
ID AAR33214 standard; protein; 3033 AA.  
DE NANBH virus strain HC-J8 protein.  
PN EP532167-A2.  
PD 17-MAR-1993.  
PA (IMMO) IMMUNO JAPAN INC.  
Query Match 6.2%; Score 73.5; DB 2; Length 3033;  
Best Local Similarity 27.4%; Pred. No. 4e+02;  
RESULT 901  
ID AAW20571 standard; protein; 114 AA.  
DE H. pylori secreted or periplasmic protein 80257.aa.  
PN WO9640893-A1.  
PD 19-DEC-1996.  
PA (ASTR) ASTRA AB.  
Query Match 6.1%; Score 73; DB 2; Length 114;  
Best Local Similarity 21.6%; Pred. No. 4.9;  
RESULT 902  
ID AAU69567 standard; protein; 189 AA.  
DE Human G protein-coupled receptor from cDNA Seq.2643.  
PN WO200177330-A2.  
PD 18-OCT-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 6.1%; Score 73; DB 5; Length 189;  
Best Local Similarity 20.3%; Pred. No. 9.8;  
RESULT 903  
ID ADC97146 standard; protein; 199 AA.  
DE E. faecium protein sequence SEQ ID 6773.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.1%; Score 73; DB 7; Length 199;  
Best Local Similarity 22.6%; Pred. No. 11;  
RESULT 904  
ID ABP29367 standard; protein; 249 AA.  
DE Streptococcus polypeptide SEQ ID NO 7910.  
PN WO200334771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.1%; Score 73; DB 5; Length 249;  
Best Local Similarity 24.6%; Pred. No. 14;  
RESULT 905  
ID AAU87836 standard; protein; 272 AA.  
DE T. aureum 7091 elongase TEL01 from plasmid pRAT-4-A1.  
PN WO200208401-A2.  
PD 31-JAN-2002.  
PA (ABBO) ABBOTT LAB.  
Query Match 6.1%; Score 73; DB 5; Length 272;  
Best Local Similarity 19.9%; Pred. No. 16;  
RESULT 906  
ID ADH80191 standard; protein; 272 AA.  
DE Fungal 7091 elongase protein seq id 75.  
PN US2003163845-A1.  
PD 28-AUG-2003.  
PA (MUKR/) MUKERJI P.  
PA (LEON/) EUN-YEONG LEONARD A.  
PA (HUAN/) HUANG Y.  
PA (PERE/) PEREIRA S L.  
Query Match 6.1%; Score 73; DB 8; Length 272;  
Best Local Similarity 19.9%; Pred. No. 16;  
RESULT 907  
ID ABW73154 standard; protein; 290 AA.  
DE Staphylococcus aureus protein #2394.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.1%; Score 73; DB 6; Length 290;  
Best Local Similarity 23.4%; Pred. No. 18;  
RESULT 908  
ID ABR47464 standard; protein; 322 AA.  
DE Breast cancer associated protein sequence SEQ ID NO.160.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.1%; Score 73; DB 6; Length 322;  
Best Local Similarity 20.6%; Pred. No. 21;  
RESULT 909  
ID ADM61865 standard; protein; 349 AA.  
DE Human novel protein NOV42a.  
PN US2004043382-A1.  
PD 04-MAR-2004.  
PA (PADI/) PADIGARU M.  
PA (SPYT/) SPYTEK K A.  
PA (SHEN/) SHENOY S G.  
PA (TAUP/) TAUPIER R J.  
PA (PENA/) PENA C E A.  
PA (LILL/) LI L.  
PA (ZERR/) ZERRHUSEN B D.  
PA (GUSE/) GUSEV V Y.  
PA (JIWU/) JI W.  
PA (GORM/) GORMAN L.  
PA (MILL/) MILLER C E.  
PA (KEXU/) KEXUDA R.  
PA (PATY/) PATTURAJAN M.  
PA (GANG/) GANGOLI E A.  
PA (VERN/) VERNET C A M.  
PA (GUOX/) GUO X S.  
PA (TCHE/) TCHERNEY V T.  
PA (FERN/) FERNANDES B R.  
PA (CASW/) CASMAN S J.  
PA (MALY/) MALYANKAR U M.  
PA (GERL/) GERLACH V.  
PA (LITV/) LITV Y.  
PA (ANDE/) ANDERSON D W.  
PA (SPAD/) SPADERNA S K.  
PA (CATY/) CATTERTON E.  
PA (LEIT/) LEITE M W.  
PA (ZHON/) ZHONG H.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLAT D M.  
PA (RIEG/) RIEGER D K.

PA (BURG/) BURGESS C E. 6.1%; Score 73; DB 8; Length 349;  
 Query Match  
 Best Local Similarity 24.0%; Pred. No. 23;  
 RESULT 910  
 ID AAM19613 standard; protein; 364 AA.  
 DE Rat growth hormone secretagogue receptor type 1a.  
 PN W09722004-A1.  
 PD 19-JUN-1997.  
 PA (MERI) MERCK & CO INC. 6.1%; Score 73; DB 2; Length 364;  
 Query Match  
 Best Local Similarity 19.4%; Pred. No. 24;  
 RESULT 911  
 ID AAY54565 standard; protein; 364 AA.  
 DE A mouse growth hormone secretagogue receptor.  
 PN W0200002818-A1.  
 PD 20-JAN-2000.  
 PA (MERI) MERCK & CO INC. 6.1%; Score 73; DB 3; Length 364;  
 Query Match  
 Best Local Similarity 19.4%; Pred. No. 24;  
 RESULT 912  
 ID AAB97377 standard; protein; 364 AA.  
 DE Rat growth hormone secretagogue receptor (GHSR) related protein.  
 PN W0200132705-A1.  
 PD 10-MAY-2001.  
 PA (TAKA) TAKEDA CHEM IND LTD. 6.1%; Score 73; DB 4; Length 364;  
 Query Match  
 Best Local Similarity 19.4%; Pred. No. 24;  
 RESULT 913  
 ID ADO29026 standard; protein; 364 AA.  
 DE Mouse novel GPCR GHSR, SEQ ID NO:125.  
 PN W02004040000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIMAL INC. 6.1%; Score 73; DB 8; Length 364;  
 Query Match  
 Best Local Similarity 19.4%; Pred. No. 24;  
 RESULT 914  
 ID AAM77773 standard; protein; 377 AA.  
 DE Staphylococcus aureus protein of unknown function.  
 PN EF841394-A2.  
 PD 13-MAY-1998.  
 PA (SMIK) SMITHKLINE BEECHAM CORP. 6.1%; Score 73; DB 2; Length 377;  
 Query Match  
 Best Local Similarity 23.3%; Pred. No. 26;  
 RESULT 915  
 ID AAG50065 standard; protein; 415 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63404.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 19.8%; Pred. No. 29;  
 RESULT 916  
 ID AAG24013 standard; protein; 427 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 27528.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 22.0%; Pred. No. 30;  
 RESULT 917  
 ID AAG24012 standard; protein; 430 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 27527.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 22.0%; Pred. No. 31;  
 RESULT 918  
 ID ABBU3419 standard; protein; 453 AA.  
 DE Protein encoded by Prokaryotic essential gene #16946.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. 6.1%; Score 73; DB 6; Length 453;  
 Query Match  
 Best Local Similarity 26.5%; Pred. No. 33;

RESULT 919  
 ID AAG50064 standard; protein; 472 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63403.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 19.8%; Pred. No. 35;  
 RESULT 920  
 ID AAG50063 standard; protein; 474 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63402.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 19.8%; Pred. No. 35;  
 RESULT 921  
 ID AAM70313 standard; protein; 490 AA.  
 DE Photoreceptor rhodopsin protein sequence #3410.  
 PN W0200294867-A2.  
 PD 28-NOV-2002.  
 PA (INSP) INST PASTEUR. 6.1%; Score 73; DB 3; Length 474;  
 Query Match  
 Best Local Similarity 24.6%; Pred. No. 37;  
 RESULT 922  
 ID AAY33766 standard; protein; 495 AA.  
 DE hKv5.1 human brain-specific potassium channel.  
 PN W09941372-A1.  
 PD 19-AUG-1999.  
 PA (ZENB) ZENCA LTD. 6.1%; Score 73; DB 2; Length 495;  
 Query Match  
 Best Local Similarity 23.2%; Pred. No. 37;  
 RESULT 923  
 ID ABO63300 standard; protein; 501 AA.  
 DE Klebsiella pneumoniae polypeptide seqid 9817.  
 PN W6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. 6.1%; Score 73; DB 7; Length 501;  
 Query Match  
 Best Local Similarity 26.5%; Pred. No. 38;  
 RESULT 924  
 ID ABB55583 standard; protein; 526 AA.  
 DE Human NOV13b protein SEQ ID NO:30.  
 PN W0200262999-A2.  
 PD 15-AUG-2002.  
 PA (CURA-) CURAGEN CORP. 6.1%; Score 73; DB 5; Length 526;  
 Query Match  
 Best Local Similarity 23.3%; Pred. No. 41;  
 RESULT 925  
 ID ADH42229 standard; protein; 526 AA.  
 DE Novel human protein NOV50d.  
 PN W02003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP. 6.1%; Score 73; DB 8; Length 526;  
 Query Match  
 Best Local Similarity 23.3%; Pred. No. 41;  
 RESULT 926  
 ID ABBU3136 standard; protein; 553 AA.  
 DE Protein encoded by Prokaryotic essential gene #16663.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. 6.1%; Score 73; DB 6; Length 553;  
 Query Match  
 Best Local Similarity 19.6%; Pred. No. 44;  
 RESULT 927  
 ID AAG24011 standard; protein; 556 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 27526.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 22.0%; Pred. No. 44;  
 RESULT 928  
 ID ADO96000 standard; protein; 608 AA.  
 DE T cell activation associated protein #89.



PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 6.1%; Score 73; DB 8; Length 608;  
Best Local Similarity 19.5%; Pred. No. 50;  
RESULT 929  
ID ADR99134 standard; protein; 635 AA.  
DE Human protein similar to Yeast SSM4, TEB4, SEQ ID 140.  
PN W02004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 6.1%; Score 73; DB 8; Length 635;  
Best Local Similarity 19.5%; Pred. No. 53;  
RESULT 930  
ID ABB71311 standard; protein; 717 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.1%; Score 73; DB 4; Length 717;  
Best Local Similarity 21.3%; Pred. No. 62;  
RESULT 931  
ID AAM26673 standard; protein; 746 AA.  
DE Staphylococcus aureus spoilin protein.  
PN W09726338-A1.  
PD 24-JUL-1997.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 6.1%; Score 73; DB 2; Length 746;  
Best Local Similarity 23.3%; Pred. No. 66;  
RESULT 932  
ID AAU37199 standard; protein; 748 AA.  
DE Staphylococcus aureus cellular proliferation protein #1369.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 4; Length 748;  
Best Local Similarity 23.3%; Pred. No. 66;  
RESULT 933  
ID AAM88407 standard; protein; 750 AA.  
DE Human adult neural tissue secreted protein s195\_10.  
PN W09857976-A1.  
PD 23-DEC-1998.  
PA (GEMY) GENETICS INST INC.  
Query Match 6.1%; Score 73; DB 2; Length 750;  
Best Local Similarity 19.5%; Pred. No. 66;  
RESULT 934  
ID AAM26672 standard; protein; 788 AA.  
DE Staphylococcus aureus spoilin protein.  
PN W09726338-A1.  
PD 24-JUL-1997.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 6.1%; Score 73; DB 2; Length 788;  
Best Local Similarity 23.3%; Pred. No. 71;  
RESULT 935  
ID AAU42392 standard; protein; 788 AA.  
DE Protein encoded by Prokaryotic essential gene #27919.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 6; Length 788;  
Best Local Similarity 23.3%; Pred. No. 71;  
RESULT 936  
ID AAU36734 standard; protein; 792 AA.  
DE Staphylococcus aureus cellular proliferation protein #904.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 4; Length 792;  
Best Local Similarity 23.3%; Pred. No. 72;  
RESULT 937  
ID ABL19057 standard; protein; 792 AA.  
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 334.  
PN W0200259148-A2.

PD 01-AUG-2002.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
Query Match 6.1%; Score 73; DB 6; Length 792;  
Best Local Similarity 23.3%; Pred. No. 72;  
RESULT 938  
ID AAM73117 standard; protein; 792 AA.  
DE Staphylococcus aureus protein #2357.  
PN W0200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.1%; Score 73; DB 6; Length 792;  
Best Local Similarity 23.3%; Pred. No. 72;  
RESULT 939  
ID AAM68466 standard; protein; 845 AA.  
DE Protein encoded by fragment #6 isolated from Hepatitis C virus genome.  
PN W09825960-A1.  
PD 18-JUN-1998.  
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
Query Match 6.1%; Score 73; DB 2; Length 845;  
Best Local Similarity 26.2%; Pred. No. 78;  
RESULT 940  
ID ADO95946 standard; protein; 910 AA.  
DE T cell activation associated protein #62.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 6.1%; Score 73; DB 8; Length 910;  
Best Local Similarity 19.5%; Pred. No. 87;  
RESULT 941  
ID AAG24246 standard; protein; 913 AA.  
DE Novel human diagnostic protein #24237.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 73; DB 4; Length 913;  
Best Local Similarity 19.5%; Pred. No. 87;  
RESULT 942  
ID AAM51861 standard; protein; 966 AA.  
DE Murine polycystic kidney disease protein 2.  
PN W0200177331-A1.  
PD 18-OCT-2001.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.1%; Score 73; DB 5; Length 966;  
Best Local Similarity 21.3%; Pred. No. 94;  
RESULT 943  
ID ABB07819 standard; protein; 966 AA.  
DE Mouse polycystic kidney disease protein 2.  
PN US2002035056-A1.  
PD 21-MAR-2002.  
PA (CURT/) CURTIS R A J.  
Query Match 6.1%; Score 73; DB 5; Length 966;  
Best Local Similarity 21.3%; Pred. No. 94;  
RESULT 944  
ID ADU76159 standard; protein; 966 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1411.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 6.1%; Score 73; DB 8; Length 966;  
Best Local Similarity 21.3%; Pred. No. 94;  
RESULT 945  
ID AAG05866 standard; protein; 971 AA.  
DE Novel human diagnostic protein #5857.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 73; DB 4; Length 971;  
Best Local Similarity 19.5%; Pred. No. 95;  
RESULT 946  
ID ADR99135 standard; protein; 971 AA.  
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 141.  
PN W02004078035-A2.

PD 16-SEP-2004.  
PA (FARB ) BAYER PHARM CORP.  
Query Match 6.1%; Score 73; DB 8; Length 971;  
Best Local Similarity 19.5%; Pred. No. 95;  
RESULT 947  
ID ABG07373 standard; protein; 976 AA.  
DE Novel human diagnostic protein #7364.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 73; DB 4; Length 976;  
Best Local Similarity 19.5%; Pred. No. 96;  
RESULT 948  
ID ABU05456 standard; protein; 209 AA.  
DE M. tuberculosis and M. leprae marker protein #107.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP ) INST PASTEUR.  
Query Match 6.1%; Score 72.5; DB 5; Length 209;  
Best Local Similarity 22.1%; Pred. No. 13;  
RESULT 949  
ID ABU15302 standard; protein; 222 AA.  
DE Protein encoded by Prokaryotic essential gene #829.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 72.5; DB 6; Length 222;  
Best Local Similarity 20.5%; Pred. No. 14;  
RESULT 950  
ID ABB53879 standard; protein; 307 AA.  
DE Lactococcus lactis protein yf5g.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.1%; Score 72.5; DB 5; Length 307;  
Best Local Similarity 22.9%; Pred. No. 22;  
RESULT 951  
ID ABB53675 standard; protein; 325 AA.  
DE Lactococcus lactis protein ydhb.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.1%; Score 72.5; DB 5; Length 325;  
Best Local Similarity 25.9%; Pred. No. 24;  
RESULT 952  
ID ADH87677 standard; protein; 353 AA.  
DE Enterococcus faecalis polypeptide #2157.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 6.1%; Score 72.5; DB 7; Length 353;  
Best Local Similarity 21.5%; Pred. No. 27;  
RESULT 953  
ID ADH87557 standard; protein; 359 AA.  
DE Enterococcus faecalis polypeptide #2037.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 6.1%; Score 72.5; DB 7; Length 359;  
Best Local Similarity 25.0%; Pred. No. 27;  
RESULT 954  
ID AAR37264 standard; protein; 389 AA.  
DE Oxytocin receptor.  
PN EP542424-A1.  
PD 19-MAY-1993.  
PA (ROHT ) ROHTO PHARM CO LTD.  
Query Match 6.1%; Score 72.5; DB 2; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 955  
ID AAW33832 standard; protein; 389 AA.  
DE Human oxytocin receptor.  
PN EP811684-A2.  
PD 10-DEC-1997.  
PA (ROHT ) ROHTO PHARM CO LTD.  
Query Match 6.1%; Score 72.5; DB 2; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 956  
ID AAM40217 standard; protein; 389 AA.  
DE Human polypeptide SEQ ID NO 3362.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 72.5; DB 4; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 957  
ID ABR81865 standard; protein; 389 AA.  
DE Human oxytocin receptor protein SEQ ID NO:215.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 6.1%; Score 72.5; DB 6; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 958  
ID AAE38317 standard; protein; 389 AA.  
DE Human oxytocin receptor protein.  
PN WO2003064402-A1.  
PD 07-AUG-2003.  
PA (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
Query Match 6.1%; Score 72.5; DB 6; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 959  
ID ADP12125 standard; protein; 389 AA.  
DE Human oxytocin receptor (OXTR) protein SEQ ID NO:2.  
PN WO2003093816-A2.  
PD 13-NOV-2003.  
PA (FARB ) BAYER AG.  
Query Match 6.1%; Score 72.5; DB 8; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 960  
ID ADI03915 standard; protein; 389 AA.  
DE Human oxytocin receptor polypeptide.  
PN WO2004000993-A2.  
PD 31-DEC-2003.  
PA (UYOU-) UNIV QUEBEC A MONTREAL.  
PA (UYMO-) UNIV MONTREAL CENT HOSPITALIER.  
Query Match 6.1%; Score 72.5; DB 8; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 961  
ID ADO29590 standard; protein; 389 AA.  
DE Human GPCR OXTR, SEQ ID NO:692.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 6.1%; Score 72.5; DB 8; Length 389;  
Best Local Similarity 24.5%; Pred. No. 31;  
RESULT 962  
ID AAR58665 standard; protein; 448 AA.  
DE Bovine PACAP receptor type IB mature protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 6.1%; Score 72.5; DB 2; Length 448;  
Best Local Similarity 29.6%; Pred. No. 37;  
RESULT 963  
ID AAR58663 standard; protein; 476 AA.  
DE Bovine PACAP receptor type IA mature protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 6.1%; Score 72.5; DB 2; Length 476;  
Best Local Similarity 29.6%; Pred. No. 40;  
RESULT 964  
ID AAR58657 standard; protein; 485 AA.

DE Bovine PACAP receptor type 1B protein.  
PD EP618291-A2.  
PN 05-OCT-1994.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 6.1%; Score 72.5; DB 2; Length 485;  
Best Local Similarity 29.6%; Pred. No. 42;  
RESULT 965  
ID AAR58655 standard; protein; 513 AA.  
DE Bovine PACAP receptor type 1A protein.  
PD EP618291-A2.  
PN 05-OCT-1994.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 6.1%; Score 72.5; DB 2; Length 513;  
Best Local Similarity 29.6%; Pred. No. 45;  
RESULT 966  
ID ADN19765 standard; protein; 522 AA.  
DE Bacterial polypeptide #2418.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAR/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.1%; Score 72.5; DB 8; Length 522;  
Best Local Similarity 22.5%; Pred. No. 46;  
RESULT 967  
ID AD181620 standard; protein; 769 AA.  
DE C. elegans protein similar to Pfam PF00023.  
PN US2004009537-A1.  
PD 15-JAN-2004.  
PA (ROOS/) ROOS J.  
PA (STAU/) STAUDERMAN K.  
PA (VELI/) VELICELEBI G.  
Query Match 6.1%; Score 72.5; DB 8; Length 769;  
Best Local Similarity 20.2%; Pred. No. 79;  
RESULT 968  
ID ABB05429 standard; protein; 848 AA.  
DE Arabidopsis thaliana ABH1 protein SEQ ID NO:2.  
PN WO200196585-A2.  
PD 20-DEC-2001.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 6.1%; Score 72.5; DB 5; Length 848;  
Best Local Similarity 22.3%; Pred. No. 90;  
RESULT 969  
ID AAK31528 standard; protein; 848 AA.  
DE Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.  
PN WO200281696-A2.  
PD 17-OCT-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.1%; Score 72.5; DB 6; Length 848;  
Best Local Similarity 22.3%; Pred. No. 90;  
RESULT 970  
ID ABU25159 standard; protein; 851 AA.  
DE Protein encoded by Prokaryotic essential gene #10686.  
PN WO2002277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 72.5; DB 6; Length 851;  
Best Local Similarity 20.5%; Pred. No. 91;  
RESULT 971  
ID AAR34580 standard; protein; 3010 AA.  
DE Human hepatitis C virus gene encoded polypeptide.  
PN EP541089-A2.  
PD 12-MAY-1993.  
PA (SANM) SANMA KAGAKU KENKYUSHO CO.  
Query Match 6.1%; Score 72.5; DB 2; Length 3010;  
Best Local Similarity 23.7%; Pred. No. 5.2e+02;  
RESULT 972  
ID ADO96378 standard; protein; 208 AA.  
DE T cell activation associated protein #278.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAHI KASEI PHARMA CORP.  
Query Match 6.0%; Score 72; DB 8; Length 208;  
Best Local Similarity 20.8%; Pred. No. 15;  
RESULT 973  
ID ABB48543 standard; protein; 306 AA.  
DE Listeria monocytogenes protein #1247.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match 6.0%; Score 72; DB 5; Length 306;  
Best Local Similarity 21.0%; Pred. No. 25;  
RESULT 974  
ID ABU3432 standard; protein; 317 AA.  
DE Protein encoded by Prokaryotic essential gene #24959.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 72; DB 6; Length 317;  
Best Local Similarity 23.5%; Pred. No. 26;  
RESULT 975  
ID AAB53392 standard; protein; 334 AA.  
DE Human colon cancer antigen protein sequence SEQ ID NO:932.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.0%; Score 72; DB 3; Length 334;  
Best Local Similarity 28.8%; Pred. No. 28;  
RESULT 976  
ID AAY87505 standard; protein; 370 AA.  
DE Human G coupled-protein receptor, hGR3.  
PN WO200017641-A1.  
PD 30-MAR-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.0%; Score 72; DB 3; Length 370;  
Best Local Similarity 21.8%; Pred. No. 33;  
RESULT 977  
ID AAW20731 standard; protein; 375 AA.  
DE H. pylori inner membrane protein, 06cp1118orf6.  
PN WO9640893-A1.  
PD 19-DEC-1996.  
PA (ASTR) ASTRA AB.  
Query Match 6.0%; Score 72; DB 2; Length 375;  
Best Local Similarity 20.9%; Pred. No. 33;  
RESULT 978  
ID ABU19932 standard; protein; 396 AA.  
DE Protein encoded by Prokaryotic essential gene #5459.  
PN WO2002277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 72; DB 6; Length 396;  
Best Local Similarity 21.6%; Pred. No. 36;  
RESULT 979  
ID ABG25051 standard; protein; 414 AA.  
DE Novel human diagnostic protein #25042.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.0%; Score 72; DB 4; Length 414;  
Best Local Similarity 22.6%; Pred. No. 38;  
RESULT 980  
ID AAG50203 standard; protein; 427 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63592.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 72; DB 3; Length 427;  
Best Local Similarity 22.0%; Pred. No. 40;  
RESULT 981  
ID AAG50202 standard; protein; 430 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63591.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 72; DB 3; Length 430;  
Best Local Similarity 22.0%; Pred. No. 40;

RESULT 982  
ID ABM72825 standard; protein: 447 AA.  
DE Staphylococcus aureus protein #2065.  
PN W020029486-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 23.9%; Pred. No. 42; Length 447;  
RESULT 983  
ID AAB62902 standard; protein: 448 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15498.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE ) PE CORP NV.  
Query Match  
Best Local Similarity 25.1%; Pred. No. 43; Length 448;  
RESULT 984  
ID ABJ16913 standard; protein: 453 AA.  
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 59.  
PN W0200259148-A2.  
PD 01-AUG-2002.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
Query Match  
Best Local Similarity 23.9%; Pred. No. 43; Length 453;  
RESULT 985  
ID ABU16441 standard; protein: 453 AA.  
DE Protein encoded by prokaryotic essential gene #1968.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 23.9%; Pred. No. 43; Length 453;  
RESULT 986  
ID ANV73057 standard; protein: 468 AA.  
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.  
PN W02004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDISEIGN NV.  
Query Match  
Best Local Similarity 21.8%; Pred. No. 45; Length 468;  
RESULT 987  
ID AAG1637 standard; protein: 495 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16945.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 21.3%; Pred. No. 49; Length 495;  
RESULT 988  
ID AAG1637 standard; protein: 497 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16944.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 21.3%; Pred. No. 49; Length 497;  
RESULT 989  
ID AAG1636 standard; protein: 507 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16943.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 21.3%; Pred. No. 51; Length 507;  
RESULT 990  
ID ADB23568 standard; protein: 543 AA.  
DE Bacterial polypeptide #12601.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 18.6%; Pred. No. 56; Length 543;

RESULT 991  
ID ABU25738 standard; protein: 552 AA.  
DE Protein encoded by prokaryotic essential gene #11265.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 19.5%; Pred. No. 57; Length 552;  
RESULT 992  
ID AAG50201 standard; protein: 556 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63590.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 22.0%; Pred. No. 58; Length 556;  
RESULT 993  
ID ADJ69383 standard; protein: 594 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1189.  
PN W02003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match  
Best Local Similarity 20.8%; Pred. No. 63; Length 594;  
RESULT 994  
ID ABB97202 standard; protein: 696 AA.  
DE Tumour-associated antigenic target protein TAR247 SEQ ID NO:84.  
PN W02003024392-A2.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.8%; Pred. No. 79; Length 696;  
RESULT 995  
ID ABB97201 standard; protein: 696 AA.  
DE Tumour-associated antigenic target protein TAR225 SEQ ID NO:83.  
PN W02003024392-A2.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 20.8%; Pred. No. 79; Length 696;  
RESULT 996  
ID ABB81969 standard; protein: 696 AA.  
DE Human GPCR XPR1 protein SEQ ID NO:424.  
PN W0200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match  
Best Local Similarity 20.8%; Pred. No. 79; Length 696;  
RESULT 997  
ID ADB67652 standard; protein: 696 AA.  
DE Human xenotropic polytropic retrovirus receptor, SEQ ID 21.  
PN W02003072824-A1.  
PD 04-SEP-2003.  
PA (SANY ) SANKYO CO LTD.  
Query Match  
Best Local Similarity 20.8%; Pred. No. 79; Length 696;  
RESULT 998  
ID ADQ96380 standard; protein: 696 AA.  
DE T cell activation associated protein #279.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAMI KASEI PHARMA CORP.  
Query Match  
Best Local Similarity 20.8%; Pred. No. 79; Length 696;  
RESULT 999  
ID ABM69179 standard; protein: 724 AA.  
DE Photorehabus luminescens protein sequence #2276.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 21.3%; Pred. No. 83; Length 724;

RESULT 1000  
ID AAB46702 standard; protein; 741 AA.  
DE P. falciparum DNA polymerase protein fragment SEQ ID NO 11.  
PN W0200075335-A2.  
PD 14-DEC-2000.  
PA (DECO-) DECODE GENETICS BHF.  
Query Match 6.0%; Score 72; DB 4; Length 741;  
Best Local Similarity 30.4%; Pred. No. 86;  
RESULT 1001  
ID AAM47977 standard; protein; 788 AA.  
DE Human HARG.  
PN CN1315342-A.  
PD 03-OCT-2001.  
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.  
Query Match 6.0%; Score 72; DB 5; Length 788;  
Best Local Similarity 26.3%; Pred. No. 93;  
RESULT 1002  
ID ABB58917 standard; protein; 1275 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3543.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.0%; Score 72; DB 4; Length 1275;  
Best Local Similarity 19.0%; Pred. No. 1.8e+02;  
RESULT 1003  
ID AAY70064 standard; protein; 2307 AA.  
DE Recombinant fusion pHCAP-1 polypeptide.  
PN W0200008469-A1.  
PD 17-FEB-2000.  
PA (AGOU-) AGOURON PHARM INC.  
Query Match 6.0%; Score 72; DB 3; Length 2307;  
Best Local Similarity 23.6%; Pred. No. 4.1e+02;  
RESULT 1004  
ID AAY70065 standard; protein; 2307 AA.  
DE Recombinant fusion pHCAP-3 polypeptide.  
PN W0200008469-A1.  
PD 17-FEB-2000.  
PA (AGOU-) AGOURON PHARM INC.  
Query Match 6.0%; Score 72; DB 3; Length 2307;  
Best Local Similarity 23.6%; Pred. No. 4.1e+02;  
RESULT 1005  
ID AAY70066 standard; protein; 2307 AA.  
DE Recombinant fusion pHCAP-4 polypeptide.  
PN W0200008469-A1.  
PD 17-FEB-2000.  
PA (AGOU-) AGOURON PHARM INC.  
Query Match 6.0%; Score 72; DB 3; Length 2307;  
Best Local Similarity 23.6%; Pred. No. 4.1e+02;  
RESULT 1006  
ID AAM93791 standard; protein; 208 AA.  
DE Human polypeptide, SEQ ID NO: 3817.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 6.0%; Score 71.5; DB 4; Length 208;  
Best Local Similarity 25.2%; Pred. No. 17;  
RESULT 1007  
ID ADL31784 standard; protein; 208 AA.  
DE Human protein encoded by a full length cDNA clone SegID 3817.  
PN EP136543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.0%; Score 71.5; DB 8; Length 208;  
Best Local Similarity 25.2%; Pred. No. 17;  
RESULT 1008  
ID AAG56417 standard; protein; 209 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72517.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 71.5; DB 3; Length 209;  
Best Local Similarity 25.6%; Pred. No. 17;  
RESULT 1009  
ID AAG56416 standard; protein; 216 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 72516.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 71.5; DB 3; Length 216;  
Best Local Similarity 25.6%; Pred. No. 18;  
RESULT 1010  
ID AAG16922 standard; protein; 218 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17750.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 71.5; DB 3; Length 218;  
Best Local Similarity 42.4%; Pred. No. 18;  
RESULT 1011  
ID ABB53486 standard; protein; 301 AA.  
DE Lactococcus lactis protein yb1G.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.0%; Score 71.5; DB 5; Length 301;  
Best Local Similarity 26.5%; Pred. No. 28;  
RESULT 1012  
ID AAM37976 standard; protein; 342 AA.  
DE Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.  
PN W03815288-A1.  
PD 16-APR-1998.  
PA (COR-) CORNELL RES FOUND INC.  
Query Match 6.0%; Score 71.5; DB 2; Length 342;  
Best Local Similarity 22.2%; Pred. No. 34;  
RESULT 1013  
ID ADG87423 standard; protein; 348 AA.  
DE Meloidogyne incognita p1K1 protein.  
PN US2003150017-A1.  
PD 07-AUG-2003.  
PA (MESA/) MESA J R B.  
PA (GRAH/) GRAHAM M W.  
PA (PAIR/) FAIRBAIN D J.  
Query Match 6.0%; Score 71.5; DB 7; Length 348;  
Best Local Similarity 21.0%; Pred. No. 34;  
RESULT 1014  
ID ADR40542 standard; protein; 363 AA.  
DE Ovine MJA protein.  
PN US2004161823-A1.  
PD 19-AUG-2004.  
PA (PEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANTATHAN C S.  
PA (HAWK/) HAWKEN D R.  
Query Match 6.0%; Score 71.5; DB 8; Length 363;  
Best Local Similarity 23.1%; Pred. No. 36;  
RESULT 1015  
ID AAR88410 standard; protein; 366 AA.  
DE High-affinity melatonin-1a receptor.  
PN W0535320-A1.  
PD 28-DEC-1995.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
Query Match 6.0%; Score 71.5; DB 2; Length 366;  
Best Local Similarity 23.1%; Pred. No. 37;  
RESULT 1016  
ID ABU03456 standard; protein; 382 AA.  
DE Angiogenesis-associated human protein sequence #1.  
PN W0200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1017  
ID ABB58069 standard; protein; 382 AA.  
DE Human G-protein coupled receptor GAVEL.  
PN W0200295056-A2.  
PD 28-NOV-2002.  
PA (AVET-) AVENTIS PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;

RESULT 1018  
ID ABR59277 standard; protein; 382 AA.  
DE Human Edg1 receptor.  
PN WO2003006503-A1.  
PD 23-JAN-2003.  
PA (CERE-) CERETEK.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1019  
ID AB008809 standard; protein; 382 AA.  
DE Human EDG-1 protein.  
PN US2002155512-A1.  
PD 24-OCT-2002.  
PA (RIGR-) RIGEL PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1020  
ID ABR59701 standard; protein; 382 AA.  
DE Human endothelial differentiation sphingolipid GPCR 1.  
PN WO2003029277-A2.  
PD 10-APR-2003.  
PA (RIGR-) RIGEL PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1021  
ID ABR81876 standard; protein; 382 AA.  
DE Human sphingolipid receptor Edg1 protein SEQ ID NO:237.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFE SPAN BIOSCIENCES INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1022  
ID ADB67662 standard; protein; 382 AA.  
DE Human EDG1, SEQ ID 31.  
PN WO2003072824-A1.  
PD 04-SEP-2003.  
PA (SANY) SANKYO CO LTD.  
Query Match 6.0%; Score 71.5; DB 7; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1023  
ID ADC40477 standard; protein; 382 AA.  
DE Protein of human EDG-1.  
PN WO2003052096-A1.  
PD 26-JUN-2003.  
PA (TAKA) TAKEDA CHEM IND LTD.  
Query Match 6.0%; Score 71.5; DB 7; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1024  
ID ADN36884 standard; protein; 382 AA.  
DE Cancer/angiogenesis/fibroblast-related polypeptide, SEQ ID NO:2.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.0%; Score 71.5; DB 7; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1025  
ID ABM85457 standard; protein; 382 AA.  
DE Human protein sequence hCPL650135.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGES DISCOVERY.  
Query Match 6.0%; Score 71.5; DB 7; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1026  
ID ADJ45541 standard; protein; 382 AA.  
DE LXR-1 ligand induced transcript seq id 72.  
PN US2004023276-A1.  
PD 05-FEB-2004.  
PA (WARD/) WARD T R.  
PA (MAOM/) MAO M.  
PA (LINS/) LINSLEY P S.  
PA (LUND/) LUND E.

Query Match 6.0%; Score 71.5; DB 8; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1027  
ID ADRE7022 standard; protein; 382 AA.  
DE Human cancer associated protein sequence SEQ ID NO:68.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGES DISCOVERY INC.  
Query Match 6.0%; Score 71.5; DB 8; Length 382;  
Best Local Similarity 22.3%; Pred. No. 39;  
RESULT 1028  
ID ADN19614 standard; protein; 383 AA.  
DE Bacterial polypeptide #2267.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOT/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.0%; Score 71.5; DB 8; Length 383;  
Best Local Similarity 22.0%; Pred. No. 39;  
RESULT 1029  
ID ABB05226 standard; protein; 390 AA.  
DE Catostomus commersoni isotocin receptor protein SEQ ID NO:3.  
PN WO200192296-A2.  
PD 06-DEC-2001.  
PA (FARB) BAYER AG.  
Query Match 6.0%; Score 71.5; DB 5; Length 390;  
Best Local Similarity 22.2%; Pred. No. 40;  
RESULT 1030  
ID ADM81141 standard; protein; 394 AA.  
DE Rat vesicle membrane protein (VMP)2.  
PN US2003175787-A1.  
PD 18-SEP-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 6.0%; Score 71.5; DB 7; Length 394;  
Best Local Similarity 22.7%; Pred. No. 41;  
RESULT 1031  
ID ABB48023 standard; protein; 435 AA.  
DE Listeria monocytogenes protein #727.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INSE PASTEUR.  
Query Match 6.0%; Score 71.5; DB 5; Length 435;  
Best Local Similarity 21.4%; Pred. No. 47;  
RESULT 1032  
ID AAR2200 standard; protein; 441 AA.  
DE Partial M17 antigen from Region II, encoded by PCR prod.  
PN WO9203457-A.  
PD 05-MAR-1992.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 6.0%; Score 71.5; DB 2; Length 441;  
Best Local Similarity 22.6%; Pred. No. 48;  
RESULT 1033  
ID ABR75877 standard; protein; 470 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 1061.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 470;  
Best Local Similarity 22.4%; Pred. No. 52;  
RESULT 1034  
ID ABU26033 standard; protein; 524 AA.  
DE Protein encoded by Prokaryotic essential gene #11560.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 524;  
Best Local Similarity 26.6%; Pred. No. 61;  
RESULT 1035  
ID ABJ37074 standard; protein; 565 AA.  
DE Human breast cancer / ovarian cancer related protein #50.

PN W02003000012-A2.  
PD 03-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 565;  
Best Local Similarity 22.4%; Pred. No. 67;  
RESULT 1036  
ID AAW51244 standard; protein; 568 AA.  
DE Human calcitonin receptor.  
PN W09821242-A1.  
PD 22-MAY-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.0%; Score 71.5; DB 2; Length 568;  
Best Local Similarity 22.4%; Pred. No. 68;  
RESULT 1037  
ID ABU16392 standard; protein; 603 AA.  
DE Protein encoded by Prokaryotic essential gene #1919.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 603;  
Best Local Similarity 21.3%; Pred. No. 74;  
RESULT 1038  
ID ABM72619 standard; protein; 603 AA.  
DE Staphylococcus aureus protein #1859.  
PN W0200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.0%; Score 71.5; DB 6; Length 603;  
Best Local Similarity 21.3%; Pred. No. 74;  
RESULT 1039  
ID ADM43215 standard; protein; 697 AA.  
DE Human methionine synthase reductase del Arg 559 variant.  
PN US2003082676-A1.  
PD 01-MAY-2003.  
PA (GRAV/) GRAVEL R A.  
PA (ROZE/) ROZEN R.  
PA (LECL/) LECLEERC D.  
PA (WILS/) WILSON A.  
PA (ROSE/) ROSENBLATT D.  
Query Match 6.0%; Score 71.5; DB 7; Length 697;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1040  
ID ADM43117 standard; protein; 697 AA.  
DE Human methionine synthase reductase del Leu 576 variant.  
PN US2003082676-A1.  
PD 01-MAY-2003.  
PA (GRAV/) GRAVEL R A.  
PA (ROZE/) ROZEN R.  
PA (LECL/) LECLEERC D.  
PA (WILS/) WILSON A.  
PA (ROSE/) ROSENBLATT D.  
Query Match 6.0%; Score 71.5; DB 7; Length 697;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1041  
ID AAB07591 standard; protein; 698 AA.  
DE A human methionine synthase reductase polypeptide.  
PN W0200042196-A2.  
PD 20-JUL-2000.  
PA (UYMC-) UNIV MCGILL.  
Query Match 6.0%; Score 71.5; DB 3; Length 698;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1042  
ID ABG00883 standard; protein; 698 AA.  
DE Novel human diagnostic protein #874.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSR-) HYSER INC.  
Query Match 6.0%; Score 71.5; DB 4; Length 698;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1043  
ID ADM43211 standard; protein; 698 AA.  
DE Human methionine synthase reductase Metc221le variant.  
PN US2003082676-A1.

PD 01-MAY-2003.  
PA (GRAV/) GRAVEL R A.  
PA (ROZE/) ROZEN R.  
PA (LECL/) LECLEERC D.  
PA (WILS/) WILSON A.  
PA (ROSE/) ROSENBLATT D.  
Query Match 6.0%; Score 71.5; DB 7; Length 698;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1044  
ID ADM43213 standard; protein; 698 AA.  
DE Human methionine synthase reductase Cys37Tyr variant.  
PN US2003082676-A1.  
PD 01-MAY-2003.  
PA (GRAV/) GRAVEL R A.  
PA (ROZE/) ROZEN R.  
PA (LECL/) LECLEERC D.  
PA (WILS/) WILSON A.  
PA (ROSE/) ROSENBLATT D.  
Query Match 6.0%; Score 71.5; DB 7; Length 698;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1045  
ID ADM43207 standard; protein; 698 AA.  
DE Human wild-type methionine synthase reductase.  
PN US2003082676-A1.  
PD 01-MAY-2003.  
PA (GRAV/) GRAVEL R A.  
PA (ROZE/) ROZEN R.  
PA (LECL/) LECLEERC D.  
PA (WILS/) WILSON A.  
PA (ROSE/) ROSENBLATT D.  
Query Match 6.0%; Score 71.5; DB 7; Length 698;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1046  
ID ADM43207 standard; protein; 698 AA.  
DE Human wild-type methionine synthase reductase.  
PN US2003082676-A1.  
PD 01-MAY-2003.  
PA (GRAV/) GRAVEL R A.  
PA (ROZE/) ROZEN R.  
PA (LECL/) LECLEERC D.  
PA (WILS/) WILSON A.  
PA (ROSE/) ROSENBLATT D.  
Query Match 6.0%; Score 71.5; DB 7; Length 698;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1047  
ID ADM43207 standard; protein; 698 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1520.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.0%; Score 71.5; DB 8; Length 698;  
Best Local Similarity 22.8%; Pred. No. 90;  
RESULT 1048  
ID ADM43207 standard; protein; 698 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1521.  
PN W02004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 6.0%; Score 71.5; DB 8; Length 725;  
Best Local Similarity 22.8%; Pred. No. 95;  
RESULT 1049  
ID AAY51606 standard; protein; 890 AA.  
DE Human wml protein.  
PN DE19845277-Cl.  
PD 09-MAR-2000.  
PA (UYMC-) UNIV MCGILL.  
Query Match 6.0%; Score 71.5; DB 3; Length 890;  
Best Local Similarity 23.8%; Pred. No. 1.3e+02;  
RESULT 1050  
ID ABB78282 standard; protein; 890 AA.  
DE Amino acid sequence of human wolframin polypeptide.  
PN W0200263307-A2.  
PD 15-AUG-2002.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 6.0%; Score 71.5; DB 5; Length 890;  
Best Local Similarity 23.8%; Pred. No. 1.3e+02;  
RESULT 1051  
ID ADD46013 standard; protein; 890 AA.  
DE Human Protein O76024, SEQ ID NO 11685.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 6.0%; Score 71.5; DB 7; Length 890;  
Best Local Similarity 23.8%; Pred. No. 1.3e+02;



RESULT 1051  
ID ADF63127 standard; protein; 890 AA.  
DE Human M953 protein sequence SEQ ID NO:97.  
PN WO2003083047-A2.  
PD 09-OCT-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 890;  
Pred. No. 1.3e+02;  
RESULT 1052  
ID ADL2689 standard; protein; 2245 AA.  
DE Human disease detection and treatment (MDPT) protein - SEQ ID 138.  
PN WO2003063379-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2245;  
Pred. No. 4.6e+02;  
RESULT 1053  
ID AAB4292 standard; protein; 2405 AA.  
DE Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 3; Length 2405;  
Pred. No. 5e+02;  
RESULT 1054  
ID ABB11404 standard; peptide; 2560 AA.  
DE Human FLAMINGO 1 homologue, SEQ ID NO:1774.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 2560;  
Pred. No. 5.5e+02;  
RESULT 1055  
ID ABL1556 standard; protein; 2894 AA.  
DE Human MDP1 polypeptide SEQ ID 503.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 2894;  
Pred. No. 6.5e+02;  
RESULT 1056  
ID AAU07054 standard; protein; 2923 AA.  
DE Human Flamingo protein encoded by cDNA splice variant.  
PN WO200161003-A1.  
PD 23-AUG-2001.  
PA (SMIX) SMITHKLINE BEECHAM PLC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1057  
ID AAM5086 standard; protein; 2923 AA.  
DE Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.  
PN WO200208765-A2.  
PD 31-JAN-2002.  
PA (STRD) UNIV STANFORD.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1058  
ID ABP82018 standard; protein; 2923 AA.  
DE Human GPCR CELSR2 protein SEQ ID NO:524.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1059  
ID AOC1549 standard; protein; 2923 AA.  
DE Human cadherin EGF LAG seven-pass G-type receptor 2.  
PN US2003086934-A1.  
PD 08-MAY-2003.  
PA (BOTS/) BOTSTEIN D.  
PA (BROW/) BROWN P O.  
PA (PERO/) PEROU C M.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 3011;  
Pred. No. 6.9e+02;  
PA (RING/) RING B.  
PA (ROSS/) ROSS D.  
PA (SEIT/) SEITZ R.  
PA (VRIU/) VAN DE RIJN J M.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1060  
ID ADC86479 standard; protein; 2923 AA.  
DE Human GPCR protein SEQ ID NO:932.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1061  
ID ADE54407 standard; protein; 2923 AA.  
DE Human Protein XP\_042739, SEQ ID NO 210.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1062  
ID ADE54411 standard; protein; 2923 AA.  
DE Human Protein XP\_042739, SEQ ID NO 214.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1063  
ID ADO29245 standard; protein; 2923 AA.  
DE Human GPCR CELSR2, SEQ ID NO:346.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 2923;  
Pred. No. 6.6e+02;  
RESULT 1064  
ID AAU74826 standard; protein; 2936 AA.  
DE Human REPTR 9 protein.  
PN WO200198354-A2.  
PD 27-DEC-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 2936;  
Pred. No. 6.6e+02;  
RESULT 1065  
ID AAU07053 standard; protein; 2956 AA.  
DE Human Flamingo polypeptide.  
PN WO200161003-A1.  
PD 23-AUG-2001.  
PA (SMIX) SMITHKLINE BEECHAM PLC.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 2956;  
Pred. No. 6.7e+02;  
RESULT 1066  
ID AAR34468 standard; protein; 3011 AA.  
DE Encoded by full-length Hepatitis C virus clone UK1-B.  
PN JP05068562-A.  
PD 23-MAR-1993.  
PA (SANW) SANWA KAGAKU KENKUSHO CO.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 3011;  
Pred. No. 6.9e+02;  
RESULT 1067  
ID AAR31621 standard; protein; 3011 AA.  
DE Hepatitis C virus (HCV) polypeptide.  
PN WO9300365-A2.  
PD 07-JAN-1993.  
PA (CHIR) CHIRON CORP.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 3011;  
Pred. No. 6.9e+02;

RESULT 1068  
ID ABB67866 standard; protein; 5303 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 30390.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 5303;  
RESULT 1069  
ID ABB06793 standard; protein; 198 AA.  
DE Human transmembrane 4 protein 22 SEQ ID NO:2.  
PN CN1327990-A.  
PD 26-DEC-2001.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 5; Length 198;  
RESULT 1070  
ID ABR58398 standard; protein; 240 AA.  
DE Human NOV17a.  
PN W02003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 6; Length 240;  
RESULT 1071  
ID ABB26255 standard; protein; 295 AA.  
DE Streptococcus polypeptide SEQ ID NO 1686.  
PN W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 5; Length 295;  
RESULT 1072  
ID AAG72952 standard; protein; 310 AA.  
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.  
PN W0200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 4; Length 310;  
RESULT 1073  
ID AAR48717 standard; protein; 312 AA.  
DE G-protein coupled human interleukin-8 receptor protein.  
PN W09405695-A1.  
PD 17-MAR-1994.  
PA (UINY) UINY NEW YORK STATE.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 2; Length 312;  
RESULT 1074  
ID AAM02689 standard; peptide; 312 AA.  
DE G-protein coupled human interleukin-8 receptor.  
PN USS508384-A.  
PD 16-APR-1996.  
PA (UINY) UINY NEW YORK STATE.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 2; Length 312;  
RESULT 1075  
ID AAG72169 standard; protein; 312 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.  
PN W0200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 4; Length 312;  
RESULT 1076  
ID AAG72377 standard; protein; 312 AA.  
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2058.  
PN W0200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 4; Length 312;  
RESULT 1077  
ID ABB54394 standard; protein; 391 AA.  
DE Lactococcus lactis protein Yk11.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOME.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 5; Length 391;  
RESULT 1078  
ID ABB48413 standard; protein; 423 AA.  
DE Listeria monocytogenes protein #1117.  
PN W0200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 5; Length 423;  
RESULT 1079  
ID ADL05302 standard; protein; 423 AA.  
DE M. catarrhalis protein #1068.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 8; Length 423;  
RESULT 1080  
ID AD095142 standard; protein; 444 AA.  
DE Novel NOVX protein sequence #185.  
PN W02003040325-A2.  
PD 15-MAY-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 7; Length 444;  
RESULT 1081  
ID AD095144 standard; protein; 444 AA.  
DE Novel NOVX protein sequence #186.  
PN W02003040325-A2.  
PD 15-MAY-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 7; Length 444;  
RESULT 1082  
ID ADP29417 standard; protein; 455 AA.  
DE Human secreted protein SEQ ID #184.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 8; Length 455;  
RESULT 1083  
ID ABU19912 standard; protein; 457 AA.  
DE Protein encoded by Prokaryotic essential gene #5439.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 6; Length 457;  
RESULT 1084  
ID AD124575 standard; protein; 470 AA.  
DE Human endogenous 5HT2A serotonin receptor.  
PN US2003224442-A1.  
PD 04-DEC-2003.  
PA (BEHA) BEHAN D P.  
PA (CHAL) CHALMERS D T.  
PA (LIAM) LIAM C W.  
PA (RUSS) RUSSO J F.  
PA (THOM) THOMSEN W J.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 8; Length 470;  
RESULT 1085  
ID AAR37659 standard; protein; 471 AA.

DE Sequence encoded by cdva.  
PN WO9311257-A2.  
PD 10-JUN-1993.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Query Match 5.9%; Score 71; DB 2; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1086  
ID AAM23781 standard; protein; 471 AA.  
DE Human serotonin 5-HT2 receptor protein.  
PN US5661024-A.  
PD 26-AUG-1997.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match 5.9%; Score 71; DB 2; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1087  
ID AAM77107 standard; protein; 471 AA.  
DE Human 5-HT2A serotonin receptor.  
PN WO9838217-A1.  
PD 03-SEP-1998.  
PA (TEIT/) TEITLER M.  
PA (HERR/) HERRICK-DAVIS K.  
PA (EGAN/) EGAN C C.  
Query Match 5.9%; Score 71; DB 2; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1088  
ID AAY90640 standard; protein; 471 AA.  
DE Human G protein-coupled receptor 5HT-2A (serotonin receptor).  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 3; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1089  
ID AAY90675 standard; protein; 471 AA.  
DE Human mutant G protein-coupled receptor 5HT-2A.  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 3; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1090  
ID AAB07978 standard; protein; 471 AA.  
DE Human 5-HT2 receptor sequence.  
PN US6383762-B1.  
PD 07-MAY-2002.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match 5.9%; Score 71; DB 5; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1091  
ID ABB81765 standard; protein; 471 AA.  
DE Human 5-HT2A receptor protein SEQ ID NO:12.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 5.9%; Score 71; DB 6; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1092  
ID ADC22641 standard; protein; 471 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #32.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1093  
ID ADC22747 standard; protein; 471 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #72.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1094  
ID ADE65844 standard; protein; 471 AA.  
DE Human serotonin 2A receptor.  
PN US2003170723-A1.  
PD 11-SEP-2003.  
PA (SATO/) SATO T.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1095  
ID ADH14220 standard; protein; 471 AA.  
DE Mutated human serotonin 5HT\_2A.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAW/) LIAW C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1096  
ID ADH14114 standard; protein; 471 AA.  
DE Human serotonin 5HT\_2A.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAW/) LIAW C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1097  
ID ADL90125 standard; protein; 471 AA.  
DE Human serotonin receptor 5HT2A.  
PN US2003167476-A1.  
PD 04-SEP-2003.  
PA (CONK/) CONKLIN B R.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1098  
ID ADO29506 standard; protein; 471 AA.  
DE Human GPCR HTR2A, SEQ ID NO:608.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMM INC.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1099  
ID ADO39800 standard; protein; 471 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1463.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1100  
ID ADO39799 standard; protein; 471 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1462.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1101  
ID ADO39798 standard; protein; 471 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1461.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 60;  
RESULT 1102  
ID AAY01626 standard; protein; 478 AA.  
DE Amino acid sequence of the human 5-HT2 receptor.  
PN US5885785-A.  
PD 23-MAR-1999.  
PA (SYNA-) SYNAPTIC PHARM CORP.

Query Match 5.9%; Score 71; DB 2; Length 478;  
Best Local Similarity 23.7%; Pred. No. 61;  
RESULT 1103  
ID ABG70577 standard; protein; 480 AA.  
DE Human serotonin (5-HT2) receptor.  
PN US2002098548-A1.  
PD 25-JUL-2002.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match 5.9%; Score 71; DB 5; Length 480;  
Best Local Similarity 23.7%; Pred. No. 62;  
RESULT 1104  
ID AAM70440 standard; protein; 493 AA.  
DE Photoreducens luminescens protein sequence #3537.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 71; DB 6; Length 493;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 1105  
ID ADE56383 standard; protein; 545 AA.  
DE Rat Protein O70536, SEQ ID NO 2235.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.9%; Score 71; DB 7; Length 545;  
Best Local Similarity 22.0%; Pred. No. 73;  
RESULT 1106  
ID ADD48660 standard; protein; 545 AA.  
DE Rat Protein BAA25372, SEQ ID NO 14366.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.9%; Score 71; DB 7; Length 545;  
Best Local Similarity 22.0%; Pred. No. 73;  
RESULT 1107  
ID ADS43584 standard; protein; 546 AA.  
DE Bacterial polypeptide #22014.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 5.9%; Score 71; DB 8; Length 546;  
Best Local Similarity 26.2%; Pred. No. 74;  
RESULT 1108  
ID AAB26399 standard; protein; 559 AA.  
DE Aspergillus fumigatus essential gene protein #1057.  
PN WO200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT) ELITTA PHARM INC.  
Query Match 5.9%; Score 71; DB 6; Length 559;  
Best Local Similarity 23.1%; Pred. No. 76;  
RESULT 1109  
ID ABB35686 standard; protein; 563 AA.  
DE Fungal ZAC protein sequence #112.  
PN WO200224865-A2.  
PD 28-MAR-2002.  
PA (MICR-) MICROBIA INC.  
Query Match 5.9%; Score 71; DB 5; Length 563;  
Best Local Similarity 19.1%; Pred. No. 77;  
RESULT 1110  
ID AAB20578 standard; protein; 564 AA.  
DE Mouse OCTN3 protein SEQ ID NO:1.  
PN WO2000046368-A1.  
PD 10-AUG-2000.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.9%; Score 71; DB 3; Length 564;  
Best Local Similarity 21.4%; Pred. No. 77;  
RESULT 1111  
ID ADQ96374 standard; protein; 631 AA.  
DE T cell activation associated protein #276.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 631;  
Best Local Similarity 21.3%; Pred. No. 90;  
RESULT 1112  
ID ADQ96376 standard; protein; 631 AA.  
DE T cell activation associated protein #277.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 631;  
Best Local Similarity 21.3%; Pred. No. 90;  
RESULT 1113  
ID ABB91532 standard; protein; 676 AA.  
DE Herbicidally active polypeptide SEQ ID NO 743.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 5.9%; Score 71; DB 5; Length 676;  
Best Local Similarity 22.3%; Pred. No. 99;  
RESULT 1114  
ID AAB21800 standard; protein; 727 AA.  
DE Human HIPHM 0000029 protein.  
PN GB2365432-A.  
PD 20-FEB-2002.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 5.9%; Score 71; DB 5; Length 727;  
Best Local Similarity 24.3%; Pred. No. 1.1e+02;  
RESULT 1115  
ID ABB54636 standard; protein; 727 AA.  
DE Human NOVX polypeptide #95.  
PN WO200281498-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 71; DB 6; Length 727;  
Best Local Similarity 24.3%; Pred. No. 1.1e+02;  
RESULT 1116  
ID ADH76500 standard; protein; 727 AA.  
DE 727 amino acid human neurotransmitter transporter protein.  
PN US200321974-A1.  
PD 27-NOV-2003.  
PA (SHAR) SHARMA R.  
PA (RAMA) RAMANATHAN C S.  
PA (WEST) WESTPHAL R.  
PA (FEDE) FEDER J N.  
PA (LEEL) LEE L M.  
Query Match 5.9%; Score 71; DB 8; Length 727;  
Best Local Similarity 24.3%; Pred. No. 1.1e+02;  
RESULT 1117  
ID AAB62929 standard; protein; 744 AA.  
DE Human neurotransmitter transporter.  
PN WO2003059947-A1.  
PD 24-JUL-2003.  
PA (FARB) BAYER AG.  
Query Match 5.9%; Score 71; DB 7; Length 744;  
Best Local Similarity 24.3%; Pred. No. 1.1e+02;  
RESULT 1118  
ID ABB60052 standard; protein; 792 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6948.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 5.9%; Score 71; DB 4; Length 792;  
Best Local Similarity 17.7%; Pred. No. 1.2e+02;  
RESULT 1119  
ID AAR30616 standard; protein; 3010 AA.  
DE Polypeptide coded by Korean HCV full cDNA sequence LBCL.  
PN EP521518-A2.  
PD 07-JAN-1993.

PA (LUCK-) LUCKY LTD.  
Query Match 5.9%; Score 71; DB 2; Length 3010;  
Best Local Similarity 26.9%; Pred. No. 7.8e+02;  
RESULT 1120  
ID AAR53417 standard; protein; 3010 AA.  
DE Blood transmissible NANBHV protein.  
PN JP06105690-A.  
PD 19-APR-1994.  
PA (KAEV-) KAEVNO K.  
Query Match 5.9%; Score 71; DB 2; Length 3010;  
Best Local Similarity 26.9%; Pred. No. 7.8e+02;  
RESULT 1121  
ID ABR83573 standard; protein; 202 AA.  
DE BcrC amino acid sequence SEQ ID NO:40.  
PN WO2003057708-A2.  
PD 17-JUL-2003.  
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.  
Query Match 5.9%; Score 70.5; DB 6; Length 202;  
Best Local Similarity 26.5%; Pred. No. 21;  
RESULT 1122  
ID AAU01287 standard; protein; 218 AA.  
DE Brassica napus fatty acid desaturase, Fad3C, partial sequence.  
PN WO200125453-A2.  
PD 12-APR-2001.  
PA (MIAC-) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
Query Match 5.9%; Score 70.5; DB 4; Length 218;  
Best Local Similarity 29.3%; Pred. No. 24;  
RESULT 1123  
ID AAU97208 standard; protein; 228 AA.  
DE Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.  
PN US633776-B1.  
PD 07-MAY-2002.  
PA (DUPO-) DU FONT DE NEMOURS & CO E I.  
Query Match 5.9%; Score 70.5; DB 5; Length 228;  
Best Local Similarity 21.6%; Pred. No. 25;  
RESULT 1124  
ID ABU08333 standard; protein; 228 AA.  
DE Wheat sugar transport protein #3.  
PN US2002178468-A1.  
PD 28-NOV-2002.  
PA (ALLE-) ALLEN S M.  
PA (HITZ-) HITZ W D.  
PA (KINN-) KINNEY A J.  
PA (TING-) TINEY S V.  
Query Match 5.9%; Score 70.5; DB 6; Length 228;  
Best Local Similarity 21.6%; Pred. No. 25;  
RESULT 1125  
ID ADG47920 standard; protein; 228 AA.  
DE Wheat Arabidopsis-like sugar transport protein #3.  
PN US2002199217-A1.  
PD 26-DEC-2002.  
PA (HELE-) HELENTARIS T G.  
Query Match 5.9%; Score 70.5; DB 8; Length 228;  
Best Local Similarity 21.6%; Pred. No. 25;  
RESULT 1126  
ID ABU17430 standard; protein; 275 AA.  
DE Protein encoded by prokaryotic essential gene #2957.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70.5; DB 6; Length 275;  
Best Local Similarity 22.8%; Pred. No. 33;  
RESULT 1127  
ID ABB55033 standard; protein; 285 AA.  
DE Lactococcus lactis protein malG.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG-) INRA INST NAT RECH AGRONOMICUE.  
Query Match 5.9%; Score 70.5; DB 5; Length 285;  
Best Local Similarity 26.1%; Pred. No. 34;  
RESULT 1128  
ID ABB05467 standard; protein; 291 AA.  
DE Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.

PN JP2001321171-A.  
PD 20-NOV-2001.  
PA (WARI-) WARIISHI H.  
PA (KUBI-) KUBOTA CORP.  
Query Match 5.9%; Score 70.5; DB 5; Length 291;  
Best Local Similarity 29.4%; Pred. No. 35;  
RESULT 1129  
ID ADA35787 standard; protein; 297 AA.  
DE Acinetobacter baumannii protein #2948.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70.5; DB 6; Length 297;  
Best Local Similarity 24.1%; Pred. No. 36;  
RESULT 1130  
ID ABM70358 standard; protein; 321 AA.  
DE Photorehabdus luminescens protein sequence #3455.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70.5; DB 6; Length 321;  
Best Local Similarity 19.2%; Pred. No. 40;  
RESULT 1131  
ID ADH22355 standard; protein; 330 AA.  
DE Human receptor & membrane associated protein (REMAP) SeqIDS.  
PN WO2003104395-A2.  
PD 18-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 5.9%; Score 70.5; DB 8; Length 330;  
Best Local Similarity 24.2%; Pred. No. 42;  
RESULT 1132  
ID ADK68232 standard; protein; 343 AA.  
DE Novel NOVX protein #79.  
PN WO2003085124-A2.  
PD 16-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 70.5; DB 7; Length 343;  
Best Local Similarity 30.0%; Pred. No. 44;  
RESULT 1133  
ID ADH72226 standard; protein; 343 AA.  
DE Human protein of the invention NOV55a SEQ ID NO:1122.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 70.5; DB 8; Length 343;  
Best Local Similarity 30.0%; Pred. No. 44;  
RESULT 1134  
ID ADR49221 standard; protein; 343 AA.  
DE Human NOV10a protein.  
PN US2004162236-A1.  
PD 19-AUG-2004.  
PA (ALSO-) ALSOBROOK J.  
PA (BENT-) BENTO P.  
PA (BOLD-) BOLDOG F.  
PA (BURG-) BURGESS C.  
PA (CASM-) CASMAN S.  
PA (BOKO-) BOKOR J C.  
PA (EDIN-) EDINGER S R.  
PA (ELLE-) ELLERMAN K.  
PA (FERN-) FERNANDES B.  
PA (GERL-) GERLACH V.  
PA (GROS-) GROSSE W.  
PA (GUNT-) GUNTHER E.  
PA (GUSE-) GUSEV V.  
PA (HEYE-) HEYES M.  
PA (LEPL-) LEPELEY D.  
PA (LI L-) LI L.  
PA (MACD-) MACDOUGALL J R.  
PA (MALI-) MALYANRAN U W.  
PA (MILT-) MILLET I.  
PA (PATR-) PATURAJAN M.  
PA (PEYM-) PEYMAN J A.

PA (RAST/) RASTELLI L.  
 PA (RIEG/) RIEGER D.  
 PA (SHEN/) SHENY S.  
 PA (SHIM/) SHIMKETS R.  
 PA (SMIT/) SMITHSON G.  
 PA (STON/) STONE D.  
 PA (VERN/) VERNET C.  
 PA (VOSS/) VOSS E.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 343;  
 Pred. No. 44;  
 RESULT 1135  
 ID ADR40543 standard; protein; 363 AA.  
 DE Ovine melatonin receptor O4608 protein.  
 PN US2004161823-A1.  
 PD 19-AUG-2004.  
 PA (PEDE/) FEDER J N.  
 PA (MINT/) MINTIER G.  
 PA (RAMA/) RAMANATHAN C S.  
 PA (HAMK/) HAMKEN D R.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 363;  
 Pred. No. 48;  
 RESULT 1136  
 ID AAR69518 standard; protein; 365 AA.  
 DE Prostaglandin-EP3-9 receptor.  
 PN WO9500552-A1.  
 PD 05-JAN-1995.  
 PA (MERI/) MERCK FROSST CANADA INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 365;  
 Pred. No. 48;  
 RESULT 1137  
 ID AAB38521 standard; protein; 365 AA.  
 DE Human PTGER3 protein isoform, EP3b.  
 PN WO2003064471-A2.  
 PD 07-AUG-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 365;  
 Pred. No. 48;  
 RESULT 1138  
 ID ADI35077 standard; protein; 365 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.  
 PN US2003243393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 365;  
 Pred. No. 48;  
 RESULT 1139  
 ID ADL15689 standard; protein; 365 AA.  
 DE Human prostaglandin EP3 receptor #3.  
 PN US6670134-B1.  
 PD 30-DEC-2003.  
 PA (ALLR/) ALLERGAN INC.  
 PA (UYAR-) UNIV ARIZONA.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 365;  
 Pred. No. 48;  
 RESULT 1140  
 ID ADR67864 standard; protein; 365 AA.  
 DE Prostaglandin E2 EP3 III.  
 PN WO2004074830-A2.  
 PD 02-SEP-2004.  
 PA (FARB/) BAYER HEALTHCARE AG.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 365;  
 Pred. No. 48;  
 RESULT 1141  
 ID ADS21429 standard; protein; 366 AA.  
 DE Bacterial polypeptide #10462.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match  
 5.9%; Score 70.5; DB 8; Length 366;  
 Pred. No. 48;

Best Local Similarity 21.2%; Pred. No. 48;  
 RESULT 1142  
 ID ADF04358 standard; protein; 367 AA.  
 DE Bacterial polypeptide #471.  
 PN US6605709-B1.  
 PD 12-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 367;  
 Pred. No. 49;  
 RESULT 1143  
 ID AAE38520 standard; protein; 374 AA.  
 DE Human PTGER3 protein isoform, EP3d.  
 PN WO2003064471-A2.  
 PD 07-AUG-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 374;  
 Pred. No. 50;  
 RESULT 1144  
 ID ADI35075 standard; protein; 374 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.  
 PN US2003243393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 374;  
 Pred. No. 50;  
 RESULT 1145  
 ID AAR48711 standard; protein; 379 AA.  
 DE G-protein coupled rat serotonin 2 receptor protein.  
 PN WO9405695-A1.  
 PD 17-MAR-1994.  
 PA (UTNY/) UNIV NEW YORK STATE.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 379;  
 Pred. No. 51;  
 RESULT 1146  
 ID AAM02683 standard; peptide; 379 AA.  
 DE G-protein coupled rat serotonin 2 receptor.  
 PN US5508384-A.  
 PD 16-APR-1996.  
 PA (UTNY/) UNIV NEW YORK STATE.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 379;  
 Pred. No. 51;  
 RESULT 1147  
 ID AAR69517 standard; protein; 388 AA.  
 DE Prostaglandin-EP3-21 receptor.  
 PN WO9500552-A1.  
 PD 05-JAN-1995.  
 PA (MERI/) MERCK FROSST CANADA INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 388;  
 Pred. No. 52;  
 RESULT 1148  
 ID AAE38513 standard; protein; 388 AA.  
 DE Human PTGER3 protein isoform, EP3c.  
 PN WO2003064471-A2.  
 PD 07-AUG-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 388;  
 Pred. No. 52;  
 RESULT 1149  
 ID ADI35061 standard; protein; 388 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.  
 PN US2003243393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 388;  
 Pred. No. 52;  
 RESULT 1150  
 ID ADL15887 standard; protein; 388 AA.  
 DE Human prostaglandin EP3 receptor #2.  
 PN US6670134-B1.  
 PD 30-DEC-2003.  
 PA (ALLR/) ALLERGAN INC.  
 PA (UYAR-) UNIV ARIZONA.  
 Query Match  
 5.9%; Score 70.5; DB 8; Length 388;  
 Pred. No. 52;

Best Local Similarity 24.2%; Pred. No. 52;  
RESULT 1151  
ID AD813753 standard; protein; 388 AA.  
DE Human prostaglandin E2 EP3 II polypeptide.  
PN WO2004075813-A2.  
PD 10-SEP-2004.  
PA (PARB ) BAYER HEALTHCARE AG.  
Query Match 5.9%; Score 70.5; DB 8; Length 388;  
Best Local Similarity 24.2%; Pred. No. 52;  
RESULT 1152  
ID AAR69516 standard; protein; 390 AA.  
DE Prostaglandin-EP3-alpha receptor.  
PN WO9500552-A1.  
PD 05-JAN-1995.  
PA (MERT ) MERCK FROSST CANADA INC.  
Query Match 5.9%; Score 70.5; DB 2; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1153  
ID AAE38516 standard; protein; 390 AA.  
DE Human PTGER3 protein isoform, EP3a1.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1154  
ID AAE38517 standard; protein; 390 AA.  
DE Human PTGER3 protein isoform, EP3a2.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1155  
ID AD135067 standard; protein; 390 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1156  
ID AD135069 standard; protein; 390 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1157  
ID AD15869 standard; protein; 390 AA.  
DE Human prostaglandin EP3 receptor #4.  
PN US6670134-B1.  
PD 30-DEC-2003.  
PA (ALLR ) ALLEGAN INC.  
PA (UYAR-) UNIV ARIZONA.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1158  
ID AD15885 standard; protein; 390 AA.  
DE Human prostaglandin EP3 receptor #1.  
PN US6670134-B1.  
PD 30-DEC-2003.  
PA (ALLR ) ALLEGAN INC.  
PA (UYAR-) UNIV ARIZONA.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1159  
ID ADR70434 standard; protein; 390 AA.  
DE Human prostaglandin E2 EP3 protein.  
PN WO2004074842-A2.  
PD 02-SEP-2004.  
PA (PARB ) BAYER HEALTHCARE AG.

Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1160  
ID AD576168 standard; protein; 390 AA.  
DE Prostaglandin E2 EP3 I.  
PN WO2004075814-A2.  
PD 10-SEP-2004.  
PA (PARB ) BAYER HEALTHCARE AG.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1161  
ID AAM57411 standard; protein; 393 AA.  
DE Human prostaglandin EP3-VI receptor.  
PN JP10113185-A.  
PD 06-MAY-1998.  
PA (ONOX ) ONO PHARM CO LTD.  
Query Match 5.9%; Score 70.5; DB 2; Length 393;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1162  
ID AAE38519 standard; protein; 393 AA.  
DE Human PTGER3 protein isoform, EP3e.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 393;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1163  
ID AAE38523 standard; protein; 393 AA.  
DE Human PTGER3 protein isoform, EP3-VI.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 393;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1164  
ID AD135081 standard; protein; 393 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 393;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1165  
ID AD135073 standard; protein; 393 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 393;  
Best Local Similarity 24.2%; Pred. No. 53;  
RESULT 1166  
ID AAM57410 standard; protein; 402 AA.  
DE Human EP3-V receptor.  
PN JP10113185-A.  
PD 06-MAY-1998.  
PA (ONOX ) ONO PHARM CO LTD.  
Query Match 5.9%; Score 70.5; DB 2; Length 402;  
Best Local Similarity 24.2%; Pred. No. 55;  
RESULT 1167  
ID AAP81904 standard; protein; 402 AA.  
DE Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 5.9%; Score 70.5; DB 6; Length 402;  
Best Local Similarity 24.2%; Pred. No. 55;  
RESULT 1168  
ID AAE38522 standard; protein; 402 AA.  
DE Human PTGER3 protein isoform, EP3-V.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 402;



Best Local Similarity 24.2%; Pred. No. 55;  
 RESULT 1169  
 ID AD135079 standard; protein: 402 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.  
 PN US2003224393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 55;  
 RESULT 1170  
 ID ADO5167 standard; protein: 402 AA.  
 DE Protein #69 with increased gene expression in renal cell carcinoma.  
 PN WO2004032842-A2.  
 PD 22-APR-2004.  
 PA (VAND-) VAN ANDEL INST.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 55;  
 RESULT 1171  
 ID ADO29620 standard; protein: 402 AA.  
 DE Human GPCR PTGER3, SEQ ID NO:1722.  
 PN WO2004040000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIML INC.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 55;  
 RESULT 1172  
 ID AAB38514 standard; protein: 407 AA.  
 DE Human PTGER3 protein isoform, EP3g.  
 PN WO2003064471-A2.  
 PD 07-AUG-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 56;  
 RESULT 1173  
 ID AD135063 standard; protein: 407 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.  
 PN US2003224393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 56;  
 RESULT 1174  
 ID AAB38518 standard; protein: 425 AA.  
 DE Human PTGER3 protein isoform, EP3f.  
 PN WO2003064471-A2.  
 PD 07-AUG-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 59;  
 RESULT 1175  
 ID AD135071 standard; protein: 425 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.  
 PN US2003224393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 59;  
 RESULT 1176  
 ID AAB38515 standard; protein: 433 AA.  
 DE Human PTGER3 protein isoform, EP3h.  
 PN WO2003064471-A2.  
 PD 07-AUG-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 61;  
 RESULT 1177  
 ID AD135065 standard; protein: 433 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.  
 PN US2003224393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 61;  
 RESULT 1178  
 ID AAB38515 standard; protein: 433 AA.  
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.  
 PN US2003224393-A1.  
 PD 04-DEC-2003.  
 PA (DECO-) DECODE GENETICS EHF.  
 Query Match  
 Best Local Similarity 24.2%; Pred. No. 61;

RESULT 1178  
 ID AAW98431 standard; protein: 480 AA.  
 DE H. pylori GPO 446 protein.  
 PN WO9843478-A1.  
 PD 08-OCT-1998.  
 PA (IMMR-) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 23.1%; Pred. No. 70;  
 RESULT 1179  
 ID ABB40525 standard; protein: 499 AA.  
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.  
 PN US6380370-B1.  
 PD 30-APR-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 20.5%; Pred. No. 74;  
 RESULT 1180  
 ID ADS06092 standard; protein: 499 AA.  
 DE Staphylococcus epidermidis seqid 5387.  
 PN US2004147734-A1.  
 PD 29-JUL-2004.  
 PA (DOUC-) DOUCETTE-STAMM L.  
 PA (BUSH-) BUSH D.  
 Query Match  
 Best Local Similarity 20.5%; Pred. No. 74;  
 RESULT 1181  
 ID ABB30473 standard; protein: 521 AA.  
 DE Protein encoded by Prokaryotic essential gene #16000.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (BLIT-) BLITRA PHARM INC.  
 Query Match  
 Best Local Similarity 23.7%; Pred. No. 79;  
 RESULT 1182  
 ID AAU97213 standard; protein: 539 AA.  
 DE Wheat sugar transport protein encoded by wlk8.pk0001.all.  
 PN US6383776-B1.  
 PD 07-MAY-2002.  
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 26.0%; Pred. No. 83;  
 RESULT 1183  
 ID ABB08338 standard; protein: 539 AA.  
 DE Wheat sugar transport protein #4.  
 PN US2002178468-A1.  
 PD 28-NOV-2002.  
 PA (ALBE-) ALLEN S M.  
 PA (HITZ-) HITZ W D.  
 PA (KINN-) KINNEY A J.  
 PA (TING-) TINGEY S V.  
 Query Match  
 Best Local Similarity 26.0%; Pred. No. 83;  
 RESULT 1184  
 ID ADG47930 standard; protein: 539 AA.  
 DE Wheat Beta-vulgaris-like sugar transport protein #1.  
 PN US2002199217-A1.  
 PD 26-DEC-2002.  
 PA (HELE-) HELENTJARIS T G.  
 Query Match  
 Best Local Similarity 26.0%; Pred. No. 83;  
 RESULT 1185  
 ID ABB27418 standard; protein: 548 AA.  
 DE Protein encoded by Prokaryotic essential gene #12945.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (BLIT-) BLITRA PHARM INC.  
 Query Match  
 Best Local Similarity 24.0%; Pred. No. 85;  
 RESULT 1186  
 ID ADN22789 standard; protein: 556 AA.  
 DE Bacterial polypeptide #5442.  
 PN US2003233675-A1.

PD 18-DEC-2003.  
 PA (CAOV/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 556;  
 RESULT 1187  
 ID ADD46023 standard; protein; 599 AA.  
 DE Rat Protein P23978, SEQ ID NO 11695.  
 PN W02003016475-A2.  
 PD 27-FEB-2003.  
 PA (GENO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;  
 RESULT 1188  
 ID ASM02687 standard; protein; 599 AA.  
 DE Rattus norvegicus neuronal GABA transporter (GAT-1).  
 PN U82003143729-A1.  
 PD 31-JUL-2003.  
 PA (SYNA-) SYNAPTIC PHARM CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;  
 RESULT 1189  
 ID AAM78767 standard; protein; 600 AA.  
 DE Human protein SEQ ID NO 1429.  
 PN W0200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 4; Length 600;  
 RESULT 1190  
 ID ADJ64315 standard; protein; 662 AA.  
 DE Cartilage differentiation inhibiting protein, SEQ ID 10.  
 PN W02004013326-A1.  
 PD 12-FEB-2004.  
 PA (ASAH) ASAH KASEI KK.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 662;  
 RESULT 1191  
 ID ABB92892 standard; protein; 700 AA.  
 DE Herbicidally active polypeptide SEQ ID NO 2103.  
 PN W0200210210-A2.  
 PD 07-FEB-2002.  
 PA (FARB) BAYER AG.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 700;  
 RESULT 1192  
 ID AAB56721 standard; protein; 717 AA.  
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1299.  
 PN W0200055174-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 717;  
 RESULT 1193  
 ID ADG47941 standard; protein; 740 AA.  
 DE Arabidopsis thaliana-1like sugar transport protein #2.  
 PN U82002199217-A1.  
 PD 26-DEC-2002.  
 PA (HELE/) HELENTARIS T G.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 740;  
 RESULT 1194  
 ID AAG39555 standard; protein; 766 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48959.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 766;  
 RESULT 1195  
 ID AAG39555 standard; protein; 815 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 815;  
 RESULT 1196  
 ID AAG39553 standard; protein; 927 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 927;  
 RESULT 1197  
 ID AEP73754 standard; protein; 1026 AA.  
 DE Candida albicans essential protein SEQ ID NO 7591.  
 PN W0200253728-A2.  
 PD 11-JUL-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1026;  
 RESULT 1198  
 ID AAM17057 standard; protein; 1027 AA.  
 DE Candida albicans chitin synthase (CHS1).  
 PN W09716540-A1.  
 PD 09-MAY-1997.  
 PA (CHEM-) CHEMGENICS PHARM INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1027;  
 RESULT 1199  
 ID ADH22510 standard; protein; 1147 AA.  
 DE Human transporter & ion channel (TRICH) protein SeqID8.  
 PN W0200309344-A2.  
 PD 13-NOV-2003.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 1147;  
 RESULT 1200  
 ID ADK18350 standard; protein; 1163 AA.  
 DE Human NOVX protein #2.  
 PN W02003057854-A2.  
 PD 17-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;  
 RESULT 1201  
 ID ADM29274 standard; protein; 1163 AA.  
 DE Human novel protein NOV2b.  
 PN W02003064628-A2.  
 PD 07-AUG-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;  
 RESULT 1202  
 ID AAM53863 standard; peptide; 1780 AA.  
 DE Human gravin polypeptide.  
 PN U85741890-A.  
 PD 21-APR-1998.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1780;  
 RESULT 1203  
 ID AAB13380 standard; protein; 1780 AA.  
 DE Human gravin protein sequence.  
 PN U86090929-A.  
 PD 18-JUL-2000.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 1780;  
 RESULT 1204  
 ID AAO17365 standard; protein; 1781 AA.  
 DE Human gravin.

RESULT 1195  
 ID AAG39555 standard; protein; 815 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 815;  
 RESULT 1196  
 ID AAG39553 standard; protein; 927 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 927;  
 RESULT 1197  
 ID AEP73754 standard; protein; 1026 AA.  
 DE Candida albicans essential protein SEQ ID NO 7591.  
 PN W0200253728-A2.  
 PD 11-JUL-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1026;  
 RESULT 1198  
 ID AAM17057 standard; protein; 1027 AA.  
 DE Candida albicans chitin synthase (CHS1).  
 PN W09716540-A1.  
 PD 09-MAY-1997.  
 PA (CHEM-) CHEMGENICS PHARM INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1027;  
 RESULT 1199  
 ID ADH22510 standard; protein; 1147 AA.  
 DE Human transporter & ion channel (TRICH) protein SeqID8.  
 PN W0200309344-A2.  
 PD 13-NOV-2003.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 1147;  
 RESULT 1200  
 ID ADK18350 standard; protein; 1163 AA.  
 DE Human NOVX protein #2.  
 PN W02003057854-A2.  
 PD 17-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;  
 RESULT 1201  
 ID ADM29274 standard; protein; 1163 AA.  
 DE Human novel protein NOV2b.  
 PN W02003064628-A2.  
 PD 07-AUG-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;  
 RESULT 1202  
 ID AAM53863 standard; peptide; 1780 AA.  
 DE Human gravin polypeptide.  
 PN U85741890-A.  
 PD 21-APR-1998.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1780;  
 RESULT 1203  
 ID AAB13380 standard; protein; 1780 AA.  
 DE Human gravin protein sequence.  
 PN U86090929-A.  
 PD 18-JUL-2000.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 1780;  
 RESULT 1204  
 ID AAO17365 standard; protein; 1781 AA.  
 DE Human gravin.

PN EPI191107-A2.  
 PD 27-MAR-2002.  
 PA (SCHD ) SCHERING AG.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1781;  
 RESULT 1203  
 ID AEU03477 standard; protein; 1781 AA.  
 DE Angiogenesis-associated human protein sequence #22.  
 PN WO200279492-A2.  
 PD 10-OCT-2002.  
 PA (BOSR-) EOS BIOTECHNOLOGY INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 6; Length 1781;  
 RESULT 1206  
 ID ABB97448 standard; protein; 1783 AA.  
 DE Novel human protein SEQ ID NO: 716.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1783;  
 RESULT 1207  
 ID ABG21018 standard; protein; 1795 AA.  
 DE Novel human diagnostic protein #21009.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70.5; DB 4; Length 1795;  
 RESULT 1208  
 ID AAG34242 standard; protein; 185 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 41631.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 3; Length 185;  
 RESULT 1209  
 ID AAG34241 standard; protein; 189 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 41630.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 3; Length 189;  
 RESULT 1210  
 ID AAW44944 standard; protein; 225 AA.  
 DE Avian infectious bronchitis virus glycoprotein M.  
 PN FR2751225-A1.  
 PD 23-JAN-1998.  
 PA (INMR ) RHONE MERIEUX SA.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 2; Length 225;  
 RESULT 1211  
 ID ABO09693 standard; protein; 226 AA.  
 DE Allostercoccus citris antigenic protein SEQ ID NO:3730.  
 PN WO2003048304-A2.  
 PD 12-JUN-2003.  
 PA (AMHP ) WYETH HOLDINGS CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 6; Length 226;  
 RESULT 1212  
 ID AAG34240 standard; protein; 235 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 41629.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 3; Length 235;  
 RESULT 1213  
 ID ABB69790 standard; protein; 256 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 36162.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 4; Length 256;

Best Local Similarity 20.2%; Pred. No. 34;  
 RESULT 1214  
 ID ADS96502 standard; protein; 256 AA.  
 DE Drosophila melanogaster protein, SEQ ID 123.  
 PN WO2004039999-A2.  
 PD 13-MAY-2004.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 8; Length 256;  
 RESULT 1215  
 ID ADP05703 standard; protein; 256 AA.  
 DE Hemophilus influenzae (NTHI) protein - SEQ ID 739.  
 PN WO2004078949-A2.  
 PD 16-SEP-2004.  
 PA (CHIL-) CHILDRENS HOSPITAL INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 8; Length 256;  
 RESULT 1216  
 ID AAG53762 standard; protein; 274 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 68478.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 3; Length 274;  
 RESULT 1217  
 ID AAG53761 standard; protein; 287 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 68477.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 3; Length 287;  
 RESULT 1218  
 ID AEU5677 standard; protein; 292 AA.  
 DE Protein encoded by Prokaryotic essential gene #21204.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 6; Length 292;  
 RESULT 1219  
 ID ADK48488 standard; protein; 307 AA.  
 DE Streptococcus pneumoniae protein, Seq ID No 5003.  
 PN US6697703-B1.  
 PD 02-MAR-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 8; Length 307;  
 RESULT 1220  
 ID AAR72985 standard; protein; 333 AA.  
 DE Epsilon opioid receptor.  
 PN WO9512670-A1.  
 PD 11-MAY-1995.  
 PA (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 2; Length 333;  
 RESULT 1221  
 ID AAY90613 standard; protein; 333 AA.  
 DE Human G protein-coupled receptor GPR8.  
 PN WO200022129-A1.  
 PD 20-APR-2000.  
 PA (AREN-) ARENA PHARM INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 3; Length 333;  
 RESULT 1222  
 ID AAY90647 standard; protein; 333 AA.  
 DE Human mutant G protein-coupled receptor GPR8 (T259K).  
 PN WO200022129-A1.  
 PD 20-APR-2000.  
 PA (AREN-) ARENA PHARM INC.  
 Query Match  
 Best Local Similarity 5.9%; Score 70; DB 3; Length 333;  
 RESULT 1223  
 ID AEU01297 standard; protein; 333 AA.

DE Human G-protein receptor 8, GPR 8, mutant N127A.  
PN WO200127632-A2.  
PD 13-APR-2001.  
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.  
PA (WILL/) WILLIAMS K M.  
Query Match 5.9%; Score 70; DB 4; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1234  
ID AAU01295 standard; protein; 333 AA.  
DE Human G-protein receptor 8, GPR 8.  
PN WO200127632-A2.  
PD 13-APR-2001.  
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.  
PA (WILL/) WILLIAMS K M.  
Query Match 5.9%; Score 70; DB 4; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1225  
ID AAU01298 standard; protein; 333 AA.  
DE Human G-protein receptor 8, GPR 8, mutant T259E.  
PN WO200127632-A2.  
PD 13-APR-2001.  
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.  
PA (WILL/) WILLIAMS K M.  
Query Match 5.9%; Score 70; DB 4; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1226  
ID ABB84683 standard; protein; 333 AA.  
DE Human GPR8-11gand related protein #1.  
PN WO200198494-A1.  
PD 27-DEC-2001.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 5; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1227  
ID ABB84723 standard; protein; 333 AA.  
DE Human GPR8-11gand related protein #3.  
PN WO200198494-A1.  
PD 27-DEC-2001.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 5; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1228  
ID ABG65918 standard; protein; 333 AA.  
DE G-protein-coupled receptor related peptide #6.  
PN WO200244368-A1.  
PD 06-JUN-2002.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 5; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1229  
ID ABU61448 standard; protein; 333 AA.  
DE Screening method related protein #1.  
PN WO200293161-A1.  
PD 21-NOV-2002.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 6; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1230  
ID ABJ37874 standard; protein; 333 AA.  
DE GPR7 11gand related human protein SEQ ID NO 84.  
PN WO2002102847-A1.  
PD 27-DEC-2002.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 6; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1231  
ID ABB81897 standard; protein; 333 AA.  
DE Human G-protein-coupled receptor GPR8 protein SEQ ID NO:279.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 5.9%; Score 70; DB 6; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;

RESULT 1232  
ID ABR57245 standard; protein; 333 AA.  
DE Human GPR8 protein SEQ ID NO:84.  
PN WO2003045994-A1.  
PD 05-JUN-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1233  
ID ADC22691 standard; protein; 333 AA.  
DE Human G-protein-coupled receptor (GPCR) polypeptide #44.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1234  
ID ADC22635 standard; protein; 333 AA.  
DE Human G-protein-coupled receptor (GPCR) polypeptide #5.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1235  
ID ADC51793 standard; protein; 333 AA.  
DE Human GPR8, SEQ ID 4.  
PN WO2003057236-A1.  
PD 17-JUL-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1236  
ID ABR61545 standard; protein; 333 AA.  
DE Human GPR8 receptor polypeptide.  
PN WO2003081234-A2.  
PD 02-OCT-2003.  
PA (FARB) BAYER AG.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1237  
ID ADG41976 standard; protein; 333 AA.  
DE Human GPR8 polypeptide.  
PN JP200309867-A.  
PD 14-JAN-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1238  
ID ADH14008 standard; protein; 333 AA.  
DE Human GPR8.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1239  
ID ADH14164 standard; protein; 333 AA.  
DE Mutated human GPR8.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1240  
ID ADG12852 standard; protein; 333 AA.  
DE Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.  
PN WO2003097795-A2.  
PD 27-NOV-2003.

PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1241  
ID ADO29700 standard; protein; 333 AA.  
DE Human GPCR GPR8, SEQ ID NO:802.  
PN W0200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1242  
ID ADO31044 standard; protein; 333 AA.  
DE Human GPCR GPR8, SEQ ID NO:73.  
PN W02004041301-A1.  
PD 21-MAY-2004.  
PA (TAKE-) TAKEEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1243  
ID ADO19919 standard; protein; 333 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.  
PN W02004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1244  
ID ADS14162 standard; protein; 333 AA.  
DE Human GPR8 ligand protein Seg1d 73.  
PN W02004080485-A1.  
PD 23-SEP-2004.  
PA (TAKE-) TAKEEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 49;  
RESULT 1245  
ID ADO12854 standard; protein; 347 AA.  
DE Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.  
PN W02003097795-A2.  
PD 27-NOV-2003.  
PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 347;  
Best Local Similarity 23.6%; Pred. No. 51;  
RESULT 1246  
ID ABG30839 standard; protein; 364 AA.  
DE Human calcium channel protein.  
PN W0200252003-A2.  
PD 04-JUL-2002.  
PA (PARB-) BAYER AG.  
Query Match 5.9%; Score 70; DB 5; Length 364;  
Best Local Similarity 25.0%; Pred. No. 55;  
RESULT 1247  
ID ADG12856 standard; protein; 364 AA.  
DE Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.  
PN W02003097795-A2.  
PD 27-NOV-2003.  
PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 364;  
Best Local Similarity 23.6%; Pred. No. 55;  
RESULT 1248  
ID ADO28778 standard; protein; 364 AA.  
DE Human GPR8-enhanced receptor.  
PN US2004091946-A1.  
PD 13-MAY-2004.  
PA (OAKU/) OAKLEY R H.  
PA (BARA/) BARAK L S.  
PA (LAPO/) LAPORTE S A.  
PA (CARO/) CARON M G.  
Query Match 5.9%; Score 70; DB 8; Length 364;  
Best Local Similarity 23.6%; Pred. No. 55;  
RESULT 1249  
ID ADG12858 standard; protein; 378 AA.  
DE HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.

PN W02003097795-A2.  
PD 27-NOV-2003.  
PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 378;  
Best Local Similarity 23.6%; Pred. No. 58;  
RESULT 1250  
ID ADN49121 standard; protein; 388 AA.  
DE Mouse oxytocin receptor protein.  
PN US2004086881-A1.  
PD 06-MAY-2004.  
PA (RAMA/) RAMANATHAN C S.  
PA (GOPA/) GOPAL S.  
PA (MINT/) MINTIER G A.  
PA (FEDER/) FEDER J.  
Query Match 5.9%; Score 70; DB 8; Length 388;  
Best Local Similarity 24.8%; Pred. No. 60;  
RESULT 1251  
ID ADO29591 standard; protein; 388 AA.  
DE Mouse GPCR OXTR, SEQ ID NO:693.  
PN W0200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 5.9%; Score 70; DB 8; Length 388;  
Best Local Similarity 24.8%; Pred. No. 60;  
RESULT 1252  
ID ADA54410 standard; protein; 399 AA.  
DE Human protein, SEQ ID 1978.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELT-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.9%; Score 70; DB 6; Length 399;  
Best Local Similarity 22.9%; Pred. No. 62;  
RESULT 1253  
ID ABG99947 standard; protein; 399 AA.  
DE Human novel polypeptide #60.  
PN W0200274961-A1.  
PD 26-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70; DB 6; Length 399;  
Best Local Similarity 22.9%; Pred. No. 62;  
RESULT 1254  
ID ADC96947 standard; protein; 425 AA.  
DE E. faecium protein sequence SEQ ID 6574.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70; DB 7; Length 425;  
Best Local Similarity 25.9%; Pred. No. 68;  
RESULT 1255  
ID ADA34110 standard; protein; 470 AA.  
DE Acinetobacter baumannii protein #1271.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70; DB 6; Length 470;  
Best Local Similarity 23.5%; Pred. No. 78;  
RESULT 1256  
ID ABM67264 standard; protein; 474 AA.  
DE Photorehabilitation luminescence protein sequence #361.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 6; Length 474;  
Best Local Similarity 22.9%; Pred. No. 79;  
RESULT 1257  
ID AAB16787 standard; protein; 475 AA.  
DE Human transporter and ion channel-24 (TRICH-24) protein.  
PN W0200192304-A2.  
PD 06-DEC-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.9%; Score 70; DB 5; Length 475;

Best Local Similarity 25.0%; Pred. No. 79;  
RESULT 1258  
ID ADAB9683 standard; protein; 506 AA.  
DE Staphylococcus aureus antigenic protein #222.  
PN W02003011899-A2.  
PD 13-FEB-2003.  
PA (UYSH-) UNIV SHEPFIELD.  
PA (BIOC-) BIOSYNEXUS INC.  
Query Match 5.9%; Score 70; DB 6; Length 506;  
Best Local Similarity 20.1%; Pred. No. 87;  
RESULT 1259  
ID ABM72414 standard; protein; 506 AA.  
DE Staphylococcus aureus protein #1654.  
PN W0200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 5.9%; Score 70; DB 6; Length 506;  
Best Local Similarity 20.1%; Pred. No. 87;  
RESULT 1260  
ID AAE21176 standard; protein; 540 AA.  
DE Human TRICH-20 protein.  
PN W0200212340-A2.  
PD 14-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.9%; Score 70; DB 5; Length 540;  
Best Local Similarity 25.0%; Pred. No. 95;  
RESULT 1261  
ID AAM39017 standard; protein; 552 AA.  
DE Human polypeptide SEQ ID NO 2162.  
PN W020015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70; DB 4; Length 552;  
Best Local Similarity 25.0%; Pred. No. 98;  
RESULT 1262  
ID ABU18262 standard; protein; 602 AA.  
DE Protein encoded by Prokaryotic essential gene #3789.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70; DB 6; Length 602;  
Best Local Similarity 26.4%; Pred. No. 1.1e+02;  
RESULT 1263  
ID ABU33453 standard; protein; 637 AA.  
DE Protein encoded by Prokaryotic essential gene #18980.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70; DB 6; Length 637;  
Best Local Similarity 23.1%; Pred. No. 1.2e+02;  
RESULT 1264  
ID AAY91335 standard; protein; 640 AA.  
DE Group B streptococcus protein sequence SEQ ID NO:68.  
PN W0200006736-A2.  
PD 10-FEB-2000.  
PA (MICR-) MICROBIAL TECHNIQS LTD.  
Query Match 5.9%; Score 70; DB 3; Length 640;  
Best Local Similarity 21.4%; Pred. No. 1.2e+02;  
RESULT 1265  
ID AMM83818 standard; protein; 695 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4067.  
PN W02004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.9%; Score 70; DB 8; Length 695;  
Best Local Similarity 28.6%; Pred. No. 1.3e+02;  
RESULT 1266  
ID ADL04660 standard; protein; 767 AA.  
DE M. catarrhalis protein #426.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70; DB 8; Length 767;  
Best Local Similarity 21.3%; Pred. No. 1.5e+02;  
RESULT 1267  
ID AAR53921 standard; protein; 980 AA.  
DE HCV fusion protein corresp. to N-terminal of ORF.  
PN JP06092996-A.  
PD 05-APR-1994.  
PA (SHIM/) SHIMOTOYA K.  
Query Match 5.9%; Score 70; DB 2; Length 980;  
Best Local Similarity 24.6%; Pred. No. 2.2e+02;  
RESULT 1268  
ID ADS24062 standard; protein; 1041 AA.  
DE Bacterial polypeptide #13095.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.9%; Score 70; DB 8; Length 1041;  
Best Local Similarity 23.4%; Pred. No. 2.4e+02;  
RESULT 1269  
ID ADP07803 standard; protein; 138 AA.  
DE Human secreted protein, seq id 286.  
PN W02004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.8%; Score 69.5; DB 8; Length 138;  
Best Local Similarity 22.0%; Pred. No. 16;  
RESULT 1270  
ID ADA33664 standard; protein; 198 AA.  
DE Actinobacter baumannii protein #825.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 198;  
Best Local Similarity 23.3%; Pred. No. 27;  
RESULT 1271  
ID ADB09276 standard; protein; 201 AA.  
DE Altolococcus citilis antigenic protein SEQ ID NO:3216.  
PN W02003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP) WYETH HOLDINGS CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 201;  
Best Local Similarity 26.0%; Pred. No. 28;  
RESULT 1272  
ID AAU29449 standard; protein; 210 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #70.  
PN W0200168858-A2.  
PD 20-SEP-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 5.8%; Score 69.5; DB 4; Length 210;  
Best Local Similarity 20.9%; Pred. No. 29;  
RESULT 1273  
ID ABG60737 standard; protein; 210 AA.  
DE Novel G protein coupled receptor (NGCPR-x) #70.  
PN US2002058306-A1.  
PD 16-MAY-2002.  
PA (VOGE/) VOGELI G.  
Query Match 5.8%; Score 69.5; DB 5; Length 210;  
Best Local Similarity 20.9%; Pred. No. 29;  
RESULT 1274  
ID AAU01288 standard; protein; 218 AA.  
DE Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.  
PN W0200125453-A2.  
PD 12-APR-2001.  
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
Query Match 5.8%; Score 69.5; DB 4; Length 218;  
Best Local Similarity 29.3%; Pred. No. 31;  
RESULT 1275  
ID ADB09278 standard; protein; 247 AA.  
DE Altolococcus citilis antigenic protein SEQ ID NO:3218.  
PN W02003048304-A2.

PD 12-JUN-2003.  
PA (AMHP ) WYETH HOLDINGS CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 247;  
Best Local Similarity 26.0%; Pred. No. 37;  
RESULT 1276  
ID AAG66935 standard; protein; 253 AA.  
DE Novel G-protein coupled receptor related protein #12.  
PN W0200240539-A2.  
PD 23-MAY-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.8%; Score 69.5; DB 5; Length 253;  
Best Local Similarity 24.2%; Pred. No. 38;  
RESULT 1277  
ID ABB62542 standard; protein; 261 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 14418.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.8%; Score 69.5; DB 4; Length 261;  
Best Local Similarity 27.7%; Pred. No. 40;  
RESULT 1278  
ID ABO80446 standard; protein; 270 AA.  
DE Pseudomonas aeruginosa polypeptide #12621.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 7; Length 270;  
Best Local Similarity 22.1%; Pred. No. 42;  
RESULT 1279  
ID ADB86076 standard; protein; 296 AA.  
DE Streptomyces hygroscopicus ABC transporter.  
PN W02003082909-A1.  
PD 09-OCT-2003.  
PA (AMHP ) WYETH.  
Query Match 5.8%; Score 69.5; DB 7; Length 296;  
Best Local Similarity 21.0%; Pred. No. 47;  
RESULT 1280  
ID AAG71524 standard; protein; 308 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1205.  
PN W0200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (VEDA ) YEDA RES & DEV CO LTD.  
Query Match 5.8%; Score 69.5; DB 4; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1281  
ID ABB44525 standard; protein; 308 AA.  
DE Human GPCR3 polypeptide SEQ ID NO 9.  
PN W0200174904-A2.  
PD 11-OCT-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.8%; Score 69.5; DB 4; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1282  
ID AAU24742 standard; protein; 308 AA.  
DE Human olfactory receptor AOLFPR242.  
PN W0200168805-A2.  
PD 20-SEP-2001.  
PA (SENO-) SENOMYX INC.  
Query Match 5.8%; Score 69.5; DB 4; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1283  
ID ABP95703 standard; protein; 308 AA.  
DE Human GPCR polypeptide SEQ ID NO 216.  
PN W0200216548-A2.  
PD 28-FEB-2002.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 5.8%; Score 69.5; DB 5; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1284  
ID AAU95729 standard; protein; 308 AA.  
DE Human olfactory and pheromone G protein-coupled receptor #216.  
PN W0200224726-A2.

PD 28-MAR-2002.  
PA (CHEM-) CHEMCOM SA.  
Query Match 5.8%; Score 69.5; DB 5; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1285  
ID AAU85362 standard; protein; 308 AA.  
DE G-coupled olfactory receptor #223.  
PN W0200198526-A2.  
PD 27-DEC-2001.  
PA (SENO-) SENOMYX INC.  
Query Match 5.8%; Score 69.5; DB 5; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1286  
ID ADC86333 standard; protein; 308 AA.  
DE Human GPCR protein SEQ ID NO:786.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 5.8%; Score 69.5; DB 7; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1287  
ID ABW02126 standard; protein; 308 AA.  
DE Human GPCR3 protein.  
PN US2003195335-A1.  
PD 16-OCT-2003.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (CASM/) CASMAN S.  
PA (ALSO/) ALSOBROOK J P.  
PA (BURG/) BURGESS C E.  
PA (PADJ/) PADIGARU M.  
PA (TAYL/) TAYLOR S.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (LILL/) LI L.  
PA (SHEN/) SHENOY S.  
PA (KEKU/) KEXUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (STON/) STONE D J.  
PA (SMIT/) SMITHSON G.  
PA (MACD/) MACDOUGALL J R.  
Query Match 5.8%; Score 69.5; DB 7; Length 308;  
Best Local Similarity 20.9%; Pred. No. 50;  
RESULT 1288  
ID ABR01671 standard; protein; 316 AA.  
DE Human G protein coupled receptor SEQ ID 202.  
PN W02003000735-A2.  
PD 03-JAN-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.8%; Score 69.5; DB 6; Length 316;  
Best Local Similarity 20.9%; Pred. No. 52;  
RESULT 1289  
ID AAY35360 standard; protein; 321 AA.  
DE Chlamydia pneumoniae involved in the virulence process.  
PN W09927105-A2.  
PD 03-JUN-1999.  
PA (GEST ) GENSET.  
Query Match 5.8%; Score 69.5; DB 2; Length 321;  
Best Local Similarity 21.4%; Pred. No. 53;  
RESULT 1290  
ID ADC33485 standard; protein; 321 AA.  
DE Yeast ARV1.  
PN US6566512-B1.  
PD 20-MAY-2003.  
PA (UTCO ) UNIV COLUMBIA NEW YORK.  
Query Match 5.8%; Score 69.5; DB 7; Length 321;  
Best Local Similarity 18.8%; Pred. No. 53;  
RESULT 1291  
ID ADE37749 standard; protein; 321 AA.  
DE Yeast ARV1 (ARE-2 Required for viability).  
PN US2003186879-A1.  
PD 02-OCT-2003.



PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 5.8%; Score 69.5; DB 7; Length 321;  
Best Local Similarity 18.8%; Pred. No. 53;  
RESULT 1292  
ID AAU5139 standard; protein; 327 AA.  
DE Propionibacterium acnes immunogenic protein #14035.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.8%; Score 69.5; DB 4; Length 327;  
Best Local Similarity 25.5%; Pred. No. 54;  
RESULT 1293  
ID ABM49658 standard; protein; 327 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 327;  
Best Local Similarity 25.5%; Pred. No. 54;  
RESULT 1294  
ID ADH10684 standard; protein; 354 AA.  
DE Rat Sprague-Dawley putative GCR polypeptide.  
PN W02003104484-A1.  
PD 18-DEC-2003.  
PA (META-) METABOLEX INC.  
Query Match 5.8%; Score 69.5; DB 8; Length 354;  
Best Local Similarity 22.0%; Pred. No. 61;  
RESULT 1295  
ID AAY05489 standard; protein; 382 AA.  
DE Human EDG-2 protein sequence.  
PN W09919513-A2.  
PD 22-APR-1999.  
PA (LXRB-) LXR BIOTECHNOLOGY INC.  
Query Match 5.8%; Score 69.5; DB 2; Length 382;  
Best Local Similarity 20.2%; Pred. No. 67;  
RESULT 1296  
ID AAU00302 standard; protein; 382 AA.  
DE LPA receptor-related amino acid sequence #1.  
PN W0200112838-A2.  
PD 22-FEB-2001.  
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.  
Query Match 5.8%; Score 69.5; DB 4; Length 382;  
Best Local Similarity 20.2%; Pred. No. 67;  
RESULT 1297  
ID ABG76099 standard; protein; 382 AA.  
DE Human lysophosphatidic acid (LPA) receptor EDG-1.  
PN US6485922-B1.  
PD 26-NOV-2002.  
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 382;  
Best Local Similarity 20.2%; Pred. No. 67;  
RESULT 1298  
ID ABB47613 standard; protein; 400 AA.  
DE Listeria monocytogenes protein #317.  
PN W0200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTERUR.  
Query Match 5.8%; Score 69.5; DB 5; Length 400;  
Best Local Similarity 22.9%; Pred. No. 72;  
RESULT 1299  
ID ABU32698 standard; protein; 400 AA.  
DE Protein encoded by Prokaryotic essential gene #18225.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 400;  
Best Local Similarity 22.9%; Pred. No. 72;  
RESULT 1300  
ID ADL12060 standard; protein; 401 AA.  
DE Drosophila dmp1 protein.  
PN W02003002137-A2.  
PD 09-JAN-2003.  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
Query Match 5.8%; Score 69.5; DB 7; Length 401;  
Best Local Similarity 20.9%; Pred. No. 72;  
RESULT 1301  
ID ABB60948 standard; protein; 415 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 9636.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.8%; Score 69.5; DB 4; Length 415;  
Best Local Similarity 20.9%; Pred. No. 75;  
RESULT 1302  
ID ADL12059 standard; protein; 415 AA.  
DE Drosophila dmp1 protein.  
PN W02003002137-A2.  
PD 09-JAN-2003.  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
Query Match 5.8%; Score 69.5; DB 7; Length 415;  
Best Local Similarity 20.9%; Pred. No. 75;  
RESULT 1303  
ID ABB66992 standard; protein; 428 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 27768.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.8%; Score 69.5; DB 4; Length 428;  
Best Local Similarity 20.9%; Pred. No. 79;  
RESULT 1304  
ID ADL12058 standard; protein; 428 AA.  
DE Drosophila dmp1 protein.  
PN W02003002137-A2.  
PD 09-JAN-2003.  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
Query Match 5.8%; Score 69.5; DB 7; Length 428;  
Best Local Similarity 20.9%; Pred. No. 79;  
RESULT 1305  
ID AAY41284 standard; protein; 444 AA.  
DE ci-NN-his fusion protein encoded by plasmid pLJM6-09.  
PN W09953033-A1.  
PD 21-OCT-1999.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 5.8%; Score 69.5; DB 2; Length 444;  
Best Local Similarity 23.6%; Pred. No. 83;  
RESULT 1306  
ID AAG30875 standard; protein; 453 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36988.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69.5; DB 3; Length 453;  
Best Local Similarity 23.3%; Pred. No. 85;  
RESULT 1307  
ID ADK47327 standard; protein; 453 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 3842.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 8; Length 453;  
Best Local Similarity 24.4%; Pred. No. 85;  
RESULT 1308  
ID ADR95087 standard; protein; 461 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 3722.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 8; Length 461;  
Best Local Similarity 24.4%; Pred. No. 87;  
RESULT 1309  
ID AAG30874 standard; protein; 476 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36987.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69.5; DB 3; Length 476;  
Best Local Similarity 23.3%; Pred. No. 91;  
RESULT 1310

ID ADN22349 standard; protein; 477 AA.  
DE Bacterial polypeptide #5002.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.8%; Score 69.5; DB 8; Length 477;  
Best Local Similarity 23.5%; Pred. No. 92;  
RESULT 1311  
ID ADS28512 standard; protein; 490 AA.  
DE Bacterial polypeptide #17545.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.8%; Score 69.5; DB 8; Length 490;  
Best Local Similarity 21.2%; Pred. No. 95;  
RESULT 1312  
ID ABO61637 standard; protein; 494 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8154.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 7; Length 494;  
Best Local Similarity 22.0%; Pred. No. 96;  
RESULT 1313  
ID AAY41278 standard; protein; 500 AA.  
DE Fusion protein containing rabbit prostaglandin EPZEP3 receptor.  
PN WO9953033-A1.  
PD 21-OCT-1999.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 5.8%; Score 69.5; DB 2; Length 500;  
Best Local Similarity 23.6%; Pred. No. 98;  
RESULT 1314  
ID AAG30873 standard; protein; 503 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36986.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69.5; DB 3; Length 503;  
Best Local Similarity 23.3%; Pred. No. 99;  
RESULT 1315  
ID AAY92829 standard; protein; 535 AA.  
DE C. pneumoniae CPN100557 processed antigen.  
PN WO200024765-A2.  
PD 04-MAY-2000.  
PA (CONN-) CONNAUGHT LAB LTD.  
Query Match 5.8%; Score 69.5; DB 3; Length 535;  
Best Local Similarity 21.4%; Pred. No. 1.1e+02;  
RESULT 1316  
ID ADR13717 standard; protein; 540 AA.  
DE Amidase, SEQ ID 54.  
PN WO2004069848-A2.  
PD 19-AUG-2004.  
PA (DIVE-) DIVERSA CORP.  
Query Match 5.8%; Score 69.5; DB 8; Length 540;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1317  
ID AAY92828 standard; protein; 547 AA.  
DE C. pneumoniae CPN100557 antigen.  
PN WO200024765-A2.  
PD 04-MAY-2000.  
PA (CONN-) CONNAUGHT LAB LTD.  
Query Match 5.8%; Score 69.5; DB 3; Length 547;  
Best Local Similarity 21.4%; Pred. No. 1.1e+02;  
RESULT 1318  
ID ABU26764 standard; protein; 547 AA.  
DE Protein encoded by prokaryotic essential gene #12291.

PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 547;  
Best Local Similarity 21.4%; Pred. No. 1.1e+02;  
RESULT 1319  
ID ABU31940 standard; protein; 551 AA.  
DE Protein encoded by prokaryotic essential gene #17467.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 551;  
Best Local Similarity 23.6%; Pred. No. 1.1e+02;  
RESULT 1320  
ID AAY01650 standard; protein; 557 AA.  
DE A protein with cation transporting activity.  
PN WO9933072-A1.  
PD 18-MAR-1999.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.8%; Score 69.5; DB 2; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1321  
ID AAY83929 standard; protein; 557 AA.  
DE Human carnitine transporter protein OCTN2.  
PN WO200014210-A1.  
PD 16-MAR-2000.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.8%; Score 69.5; DB 3; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1322  
ID ABG03029 standard; protein; 557 AA.  
DE Novel human diagnostic protein #3020.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69.5; DB 4; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1323  
ID ABB82979 standard; protein; 557 AA.  
DE Human SLC22A related protein-GenBank Identifier No. GI# 3242598.  
PN WO200299053-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1324  
ID ABB82980 standard; protein; 557 AA.  
DE Human SLC22A related protein-GenBank Identifier No. GI# 4507005.  
PN WO200299053-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1325  
ID ABO07242 standard; protein; 557 AA.  
DE Human p53 modifying protein, SEQ ID 202.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1326  
ID ADE09321 standard; protein; 557 AA.  
DE Novel protein-related contig polypeptide sequence #387.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69.5; DB 7; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1327  
ID ADE09361 standard; protein; 557 AA.  
DE Novel protein-related contig polypeptide sequence #327.  
PN WO2003054152-A2.

PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69.5; DB 7; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1328  
ID ADP23817 standard; protein; 557 AA.  
DE PRO polypeptide SEQ ID NO:995.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GERTH-) GENENTECH INC.  
Query Match 5.8%; Score 69.5; DB 8; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.1e+02;  
RESULT 1329  
ID ADA34637 standard; protein; 559 AA.  
DE Acinetobacter baumannii protein #1798.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 559;  
Best Local Similarity 20.2%; Pred. No. 1.1e+02;  
RESULT 1330  
ID ABO62908 standard; protein; 564 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9425.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 7; Length 564;  
Best Local Similarity 23.6%; Pred. No. 1.2e+02;  
RESULT 1331  
ID ABB89665 standard; protein; 568 AA.  
DE Human polypeptide SEQ ID NO 2041.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.8%; Score 69.5; DB 5; Length 568;  
Best Local Similarity 22.4%; Pred. No. 1.2e+02;  
RESULT 1332  
ID ADB65515 standard; protein; 573 AA.  
DE Human protein encoded by clone TEST120271790.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.8%; Score 69.5; DB 7; Length 573;  
Best Local Similarity 22.7%; Pred. No. 1.2e+02;  
RESULT 1333  
ID ABB47410 standard; protein; 579 AA.  
DE Listeria monocytogenes protein #114.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP-) INST PASTEUR.  
Query Match 5.8%; Score 69.5; DB 5; Length 579;  
Best Local Similarity 21.1%; Pred. No. 1.2e+02;  
RESULT 1334  
ID ABB32703 standard; protein; 579 AA.  
DE Protein encoded by Prokaryotic essential gene #18230.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 579;  
Best Local Similarity 21.1%; Pred. No. 1.2e+02;  
RESULT 1335  
ID ABB65234 standard; protein; 599 AA.  
DE Hypoxia-regulated protein #108.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 5.8%; Score 69.5; DB 5; Length 599;  
Best Local Similarity 19.6%; Pred. No. 1.3e+02;  
RESULT 1336  
ID AAE38584 standard; protein; 599 AA.  
DE Human GAT1 GABA transporter protein.  
PN WO2003061573-A2.

PD 31-JUL-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 5.8%; Score 69.5; DB 7; Length 599;  
Best Local Similarity 19.6%; Pred. No. 1.3e+02;  
RESULT 1337  
ID ADD46025 standard; protein; 599 AA.  
DE Human Protein P30531, SEQ ID NO 11697.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 5.8%; Score 69.5; DB 7; Length 599;  
Best Local Similarity 19.6%; Pred. No. 1.3e+02;  
RESULT 1338  
ID AAY41285 standard; protein; 656 AA.  
DE CI-77A-TL fusion protein encoded by plasmid pLJM5-42T.  
PN WO9953033-A1.  
PD 21-OCT-1999.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 5.8%; Score 69.5; DB 2; Length 656;  
Best Local Similarity 23.6%; Pred. No. 1.4e+02;  
RESULT 1339  
ID ABB40194 standard; protein; 660 AA.  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 5; Length 660;  
Best Local Similarity 27.2%; Pred. No. 1.4e+02;  
RESULT 1340  
ID ADS07250 standard; protein; 660 AA.  
DE Staphylococcus epidermidis polypeptide seqid 6545.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC-) DODGETTE-STAMM L.  
PA (BUSH-) BUSH D.  
Query Match 5.8%; Score 69.5; DB 8; Length 660;  
Best Local Similarity 27.2%; Pred. No. 1.4e+02;  
RESULT 1341  
ID AAV17390 standard; protein; 663 AA.  
DE Human vesicle membrane protein-like protein 3.  
PN WO9921994-A2.  
PD 06-MAY-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 5.8%; Score 69.5; DB 2; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
RESULT 1342  
ID ADM83092 standard; protein; 663 AA.  
DE Human vesicle membrane protein (VMP)2.  
PN US2003175787-A1.  
PD 18-SEP-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 5.8%; Score 69.5; DB 7; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
RESULT 1343  
ID ADU64317 standard; protein; 663 AA.  
DE Cartilage differentiation inhibiting protein, SEQ ID 12.  
PN WO2004013326-A1.  
PD 12-FEB-2004.  
PA (ASAH-) ASAH KASEI KK.  
Query Match 5.8%; Score 69.5; DB 8; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
RESULT 1344  
ID ADQ96536 standard; protein; 663 AA.  
DE T cell activation associated protein #357.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 5.8%; Score 69.5; DB 8; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.4e+02;  
RESULT 1345  
ID ADO09827 standard; protein; 681 AA.  
DE Hamster SGLT homologue protein SEQ ID NO:50.

PN WO2004039405-A1.  
ID 13-MAY-2004.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 8; Length 681;  
RESULT 1346  
ID ABU41908 standard; protein; 695 AA.  
DE Protein encoded by Prokaryotic essential gene #27435.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 6; Length 695;  
RESULT 1347  
ID ADJ48367 standard; protein; 764 AA.  
DE Maize oil-associated gene protein #26.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR) LAURIE C C.  
PA (RAVA) RAVANELLO M.  
PA (SAVA) SAVAGE T.  
PA (LEDE) LEDEAUX J R.  
PA (ROGE) ROGERS J A.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 8; Length 764;  
RESULT 1348  
ID ABU43821 standard; protein; 801 AA.  
DE Protein encoded by Prokaryotic essential gene #29348.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 6; Length 801;  
RESULT 1349  
ID AAY70245 standard; protein; 805 AA.  
DE Human Polycystin-L protein.  
PN WO20012046-A2.  
PD 09-MAR-2000.  
PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 3; Length 805;  
RESULT 1350  
ID ABB98140 standard; protein; 863 AA.  
DE Human PMM incycle ID 7484157CD1.  
PN WO200246383-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 5; Length 863;  
RESULT 1351  
ID AAY96168 standard; protein; 877 AA.  
DE Saccharomyces cerevisiae OPT protein YPR194C.  
PN WO200052162-A2.  
PD 08-SEP-2000.  
PA (UTTE-) UNIV TENNESSEE RES CORP.  
PA (BECK) BECKER J M.  
PA (HAUS) HAUSER M.  
PA (DONH) DONHARDT A.  
PA (BARN) BARNES D.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 3; Length 877;  
RESULT 1352  
ID ADS4417 standard; protein; 877 AA.  
DE Bacterial polypeptide #22547.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 8; Length 877;  
22.7%; Pred. No. 2.1e+02;

RESULT 1353  
ID AAG70761 standard; protein; 881 AA.  
DE S cerevisiae apoptosis associated protein YUH197W.  
PN WO200102550-A2.  
PD 11-JAN-2001.  
PA (JANC) JANSSEN PHARM NV.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 4; Length 881;  
RESULT 1354  
ID ABU16635 standard; protein; 1010 AA.  
DE Protein encoded by Prokaryotic essential gene #2162.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 6; Length 1010;  
RESULT 1355  
ID ADA34462 standard; protein; 1028 AA.  
DE Acinetobacter Baumannii protein #1623.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 6; Length 1028;  
RESULT 1356  
ID AAM25671 standard; protein; 1684 AA.  
DE hABC3 protein.  
PN WO9702346-A2.  
PD 23-JAN-1997.  
PA (GENZ) GENZYME CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 2; Length 1684;  
RESULT 1357  
ID AAM46761 standard; protein; 1684 AA.  
DE Amino acid sequence of human ATP binding cassette transporter.  
PN WO9748797-A1.  
PD 24-DEC-1997.  
PA (GENZ) GENZYME CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 2; Length 1684;  
RESULT 1358  
ID AAM46771 standard; protein; 1704 AA.  
DE Amino acid sequence of human ATP binding cassette transporter.  
PN WO9748797-A1.  
PD 24-DEC-1997.  
PA (GENZ) GENZYME CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 2; Length 1704;  
RESULT 1359  
ID ABB52094 standard; protein; 1704 AA.  
DE Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.  
PN EP1217066-A1.  
PD 26-JUN-2002.  
PA (UYGE-) UNIV GENT.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 5; Length 1704;  
RESULT 1360  
ID ADJ70414 standard; protein; 1704 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2220.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 7; Length 1704;  
RESULT 1361  
ID ADU61289 standard; protein; 1704 AA.  
DE Human ATP-binding cassette subfamily A (ABCI) member 3 protein.  
PN WO2004020583-A2.  
PD 11-MAR-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 8; Length 1704;  
20.3%; Pred. No. 5.4e+02;

RESULT 1362  
ID AAB09274 standard; protein; 154 AA.  
DE A101ococcus otitis antigenic protein SEQ ID NO:3214.  
PN W02003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP ) WYETH HOLDINGS CORP.  
Query Match 5.8%; Score 69; DB 6; Length 154;  
Best Local Similarity 27.3%; Pred. No. 22;  
RESULT 1363  
ID ADK16543 standard; protein; 178 AA.  
DE Nanoarchaeum equitans cancer-associated (CA) protein #247.  
PN W02003093434-A2.  
PD 13-NOV-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 5.8%; Score 69; DB 8; Length 178;  
Best Local Similarity 23.3%; Pred. No. 27;  
RESULT 1364  
ID AAV65589 standard; protein; 191 AA.  
DE Propionibacterium acnes immunogenic protein #26485.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.8%; Score 69; DB 4; Length 191;  
Best Local Similarity 26.6%; Pred. No. 29;  
RESULT 1365  
ID AAM62108 standard; protein; 191 AA.  
DE Propionibacterium acnes permease/transporter-related polypeptide #26784.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.8%; Score 69; DB 6; Length 191;  
Best Local Similarity 26.6%; Pred. No. 29;  
RESULT 1366  
ID AAM38633 standard; protein; 193 AA.  
DE S. pneumoniae LPLC protein.  
PN W09743303-A1.  
PD 20-NOV-1997.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 5.8%; Score 69; DB 2; Length 193;  
Best Local Similarity 28.3%; Pred. No. 30;  
RESULT 1367  
ID AAB21047 standard; protein; 214 AA.  
DE Human nucleic acid-binding protein, NUBP-51.  
PN W0200044800-A2.  
PD 03-AUG-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 5.8%; Score 69; DB 3; Length 214;  
Best Local Similarity 24.7%; Pred. No. 34;  
RESULT 1368  
ID ABP58238 standard; protein; 214 AA.  
DE Human ovary-specific O1-236 (NPM2) protein.  
PN W0200288314-A2.  
PD 07-NOV-2002.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 5.8%; Score 69; DB 6; Length 214;  
Best Local Similarity 24.7%; Pred. No. 34;  
RESULT 1369  
ID ADJ63172 standard; protein; 214 AA.  
DE Human nucleolepialamin (Npm2) protein.  
PN W02003091400-A2.  
PD 06-NOV-2003.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 5.8%; Score 69; DB 7; Length 214;  
Best Local Similarity 24.7%; Pred. No. 34;  
RESULT 1370  
ID ADM03849 standard; protein; 214 AA.  
DE Human protein of the invention SEQ ID NO:2534.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.8%; Score 69; DB 7; Length 214;  
Best Local Similarity 24.7%; Pred. No. 34;  
RESULT 1371  
ID ADN46858 standard; protein; 239 AA.  
DE Thermococcus kodakarensis KOD1 protein sequence SegID736.  
PN W02004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 5.8%; Score 69; DB 8; Length 239;  
Best Local Similarity 23.5%; Pred. No. 40;  
RESULT 1372  
ID AAM69345 standard; protein; 337 AA.  
DE Photorhabdus luminescens protein sequence #2642.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
Query Match 5.8%; Score 69; DB 6; Length 337;  
Best Local Similarity 19.8%; Pred. No. 65;  
RESULT 1373  
ID AAM72781 standard; protein; 350 AA.  
DE Staphylococcus aureus protein #2021.  
PN W0200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 5.8%; Score 69; DB 6; Length 350;  
Best Local Similarity 20.5%; Pred. No. 68;  
RESULT 1374  
ID AAG04120 standard; protein; 356 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 356;  
Best Local Similarity 21.0%; Pred. No. 70;  
RESULT 1375  
ID AAR91218 standard; protein; 370 AA.  
DE Human pituitary G-protein coupled receptor protein.  
PN W09605302-A1.  
PD 22-FEB-1996.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 5.8%; Score 69; DB 2; Length 370;  
Best Local Similarity 21.8%; Pred. No. 74;  
RESULT 1376  
ID AAM31379 standard; protein; 370 AA.  
DE Human G-protein-coupled receptor protein from phGR3.  
PN W09724436-A2.  
PD 10-JUL-1997.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 5.8%; Score 69; DB 2; Length 370;  
Best Local Similarity 21.8%; Pred. No. 74;  
RESULT 1377  
ID AAW95181 standard; peptide; 370 AA.  
DE Human G-protein coupled receptor polypeptide.  
PN W09849235-A1.  
PD 05-NOV-1998.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 5.8%; Score 69; DB 2; Length 370;  
Best Local Similarity 21.8%; Pred. No. 74;  
RESULT 1378  
ID AAW97221 standard; peptide; 370 AA.  
DE Human pituitary-derived G-protein-coupled receptor protein.  
PN W09858962-A1.  
PD 30-DEC-1998.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 5.8%; Score 69; DB 2; Length 370;  
Best Local Similarity 21.8%; Pred. No. 74;  
RESULT 1379  
ID AAG04119 standard; protein; 370 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 370;  
Best Local Similarity 21.0%; Pred. No. 74;

RESULT 1380  
ID AAG62539 standard; protein; 370 AA.  
DE Human CRH releasing protein related protein SEQ ID NO: 46.  
PN WO200135984-A1.  
PD 25-MAY-2001.  
PA (TAKE ) TAKEEDA CHEM IND LTD.  
Query Match 5.8%; Score 69; DB 4; Length 370;  
Best Local Similarity 21.8%; Pred. No. 74;  
RESULT 1381  
ID ABB81880 standard; protein; 370 AA.  
DE Human G protein-coupled receptor 10 protein SEQ ID NO:245.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 5.8%; Score 69; DB 6; Length 370;  
Best Local Similarity 21.8%; Pred. No. 74;  
RESULT 1382  
ID ADO29365 standard; protein; 370 AA.  
DE Human GPCR GPR10, SEQ ID NO:466.  
PN WO200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 5.8%; Score 69; DB 8; Length 370;  
Best Local Similarity 21.8%; Pred. No. 74;  
RESULT 1383  
ID AAM27510 standard; protein; 380 AA.  
DE Consensus human hypothalamic receptor.  
PN WO9708317-A2.  
PD 06-MAR-1997.  
PA (CHIR ) CHIRON CORP.  
Query Match 5.8%; Score 69; DB 2; Length 380;  
Best Local Similarity 21.8%; Pred. No. 76;  
RESULT 1384  
ID AAB16020 standard; protein; 388 AA.  
DE E. coli proliferation associated protein sequence SEQ ID NO:378.  
PN WO200044506-A2.  
PD 03-AUG-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69; DB 3; Length 388;  
Best Local Similarity 27.2%; Pred. No. 79;  
RESULT 1385  
ID AAG98322 standard; protein; 388 AA.  
DE Escherichia coli protein sequence SEQ ID NO:370.  
PN WO200148209-A2.  
PD 05-JUL-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69; DB 4; Length 388;  
Best Local Similarity 27.2%; Pred. No. 79;  
RESULT 1386  
ID AAB14818 standard; protein; 388 AA.  
DE Protein encoded by Prokaryotic essential gene #345.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69; DB 6; Length 388;  
Best Local Similarity 27.2%; Pred. No. 79;  
RESULT 1387  
ID ADS45229 standard; protein; 437 AA.  
DE Bacterial polypeptide #23659.  
PN US200233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 5.8%; Score 69; DB 8; Length 437;  
Best Local Similarity 22.4%; Pred. No. 93;  
RESULT 1388  
ID ABO61901 standard; protein; 472 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8418.  
PN US6610836-B1.  
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69; DB 7; Length 472;  
Best Local Similarity 21.3%; Pred. No. 1e+02;  
RESULT 1389  
ID AAG42138 standard; protein; 508 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52514.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 508;  
Best Local Similarity 20.2%; Pred. No. 1.1e+02;  
RESULT 1390  
ID AAG04118 standard; protein; 509 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 25.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 509;  
Best Local Similarity 21.0%; Pred. No. 1.1e+02;  
RESULT 1391  
ID AAG42137 standard; protein; 520 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52513.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 520;  
Best Local Similarity 20.2%; Pred. No. 1.2e+02;  
RESULT 1392  
ID AAB59760 standard; protein; 593 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6072.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.8%; Score 69; DB 4; Length 593;  
Best Local Similarity 22.7%; Pred. No. 1.4e+02;  
RESULT 1393  
ID AAG31959 standard; protein; 609 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38469.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 609;  
Best Local Similarity 21.0%; Pred. No. 1.5e+02;  
RESULT 1394  
ID AAG31958 standard; protein; 624 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38468.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 624;  
Best Local Similarity 21.0%; Pred. No. 1.5e+02;  
RESULT 1395  
ID AAE05101 standard; protein; 641 AA.  
DE Drosophila melanogaster dmksnf.  
PN WO200149848-A2.  
PD 12-JUL-2001.  
PA (GENO-) GENOPTERA LLC.  
Query Match 5.8%; Score 69; DB 4; Length 641;  
Best Local Similarity 22.7%; Pred. No. 1.6e+02;  
RESULT 1396  
ID AAG31957 standard; protein; 659 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38467.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.8%; Score 69; DB 3; Length 659;  
Best Local Similarity 21.0%; Pred. No. 1.6e+02;  
RESULT 1397  
ID ABB11769 standard; peptide; 666 AA.  
DE Human d37C10.3 ATPase homologue, SEQ ID NO:2139.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69; DB 4; Length 666;  
Best Local Similarity 23.4%; Pred. No. 1.7e+02;  
RESULT 1398  
ID AAM79751 standard; protein; 666 AA.  
DE Human protein SEQ ID NO 3397.  
PN WO200157190-A2.

PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69; DB 4; Length 666;  
Best Local Similarity 23.4%; Pred. No. 1.7e+02;  
RESULT 1399  
ID ADF05168 standard; protein; 681 AA.  
DE Bacterial polypeptide #1281.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69; DB 7; Length 681;  
Best Local Similarity 21.5%; Pred. No. 1.7e+02;  
RESULT 1400  
ID AOC52988 standard; protein; 791 AA.  
DE Human putative spliceosome associated protein (SAP) #52.  
PN US2003068803-A1.  
PD 10-APR-2003.  
PA (REED/) REED R.  
PA (ZHOU/) ZHOU Z.  
Query Match 5.8%; Score 69; DB 6; Length 791;  
Best Local Similarity 24.8%; Pred. No. 2.1e+02;  
RESULT 1401  
ID AAB42779 standard; protein; 792 AA.  
DE Human OREX ORF2543 polypeptide sequence SEQ ID NO:5086.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.8%; Score 69; DB 3; Length 792;  
Best Local Similarity 24.8%; Pred. No. 2.1e+02;  
RESULT 1402  
ID ABB62960 standard; protein; 875 AA.  
DE Human polypeptide SEQ ID NO 397.  
PN WO200218424-A2.  
PD 07-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69; DB 5; Length 875;  
Best Local Similarity 24.8%; Pred. No. 2.4e+02;  
RESULT 1403  
ID AAM85143 standard; protein; 891 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5392.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.8%; Score 69; DB 8; Length 891;  
Best Local Similarity 19.5%; Pred. No. 2.5e+02;  
RESULT 1404  
ID ABB90877 standard; protein; 1933 AA.  
DE Hericidially active polypeptide SEQ ID NO 88.  
PN WO20020210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match 5.8%; Score 69; DB 5; Length 1933;  
Best Local Similarity 17.4%; Pred. No. 7.3e+02;  
RESULT 1405  
ID AD195303 standard; protein; 2280 AA.  
DE OSPF-related Hepatitis C virus (HCV) polypeptide.  
PN WO200402415-A2.  
PD 08-JAN-2004.  
PA (DAND-) DANA FARRER CANCER INST INC.  
Query Match 5.8%; Score 69; DB 8; Length 2280;  
Best Local Similarity 26.9%; Pred. No. 9.2e+02;  
RESULT 1406  
ID ADM68764 standard; protein; 5127 AA.  
DE Peregrinus maidis ryanodine receptor protein SEQ ID NO:8.  
PN WO2004027042-A2.  
PD 01-APR-2004.  
PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
Query Match 5.8%; Score 69; DB 8; Length 5127;  
Best Local Similarity 20.1%; Pred. No. 2.8e+03;  
RESULT 1407  
ID ADH85829 standard; protein; 178 AA.  
DE Enterococcus faecalis polypeptide #309.  
PN US6617156-B1.

PD 09-SEP-2003.  
PA (DOUC-) DOUCETTE-STAMM L A.  
PA (BUSH-) BUSH D.  
Query Match 5.7%; Score 68.5; DB 7; Length 178;  
Best Local Similarity 30.7%; Pred. No. 31;  
RESULT 1408  
ID ABJ01003 standard; protein; 209 AA.  
DE Human breast specific protein SEQ ID NO: 86.  
PN WO200240672-A2.  
PD 23-MAY-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 5.7%; Score 68.5; DB 5; Length 209;  
Best Local Similarity 21.8%; Pred. No. 38;  
RESULT 1409  
ID AAG53772 standard; protein; 218 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68492.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.7%; Score 68.5; DB 3; Length 218;  
Best Local Similarity 40.7%; Pred. No. 41;  
RESULT 1410  
ID AAG53640 standard; protein; 218 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29784.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.7%; Score 68.5; DB 3; Length 218;  
Best Local Similarity 40.7%; Pred. No. 41;  
RESULT 1411  
ID AAG53747 standard; protein; 218 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68458.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.7%; Score 68.5; DB 3; Length 218;  
Best Local Similarity 40.7%; Pred. No. 41;  
RESULT 1412  
ID ADF07413 standard; protein; 225 AA.  
DE Bacterial polypeptide #3526.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 68.5; DB 7; Length 225;  
Best Local Similarity 18.2%; Pred. No. 42;  
RESULT 1413  
ID ADO57686 standard; protein; 227 AA.  
DE Actinobacillus actinomycetemcomitans immunogenic polypeptide #68.  
PN WO2004045499-A2.  
PD 03-JUN-2004.  
PA (UYFL-) UNIV FLORIDA.  
Query Match 5.7%; Score 68.5; DB 8; Length 227;  
Best Local Similarity 24.3%; Pred. No. 43;  
RESULT 1414  
ID ADA14398 standard; protein; 278 AA.  
DE Mouse spermatogenesis related protein sequence SEQ ID NO:140.  
PN WO2003068969-A1.  
PD 21-AUG-2003.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 5.7%; Score 68.5; DB 6; Length 278;  
Best Local Similarity 29.2%; Pred. No. 57;  
RESULT 1415  
ID ABU29281 standard; protein; 322 AA.  
DE Protein encoded by Prokaryotic essential gene #14808.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.7%; Score 68.5; DB 6; Length 322;  
Best Local Similarity 30.7%; Pred. No. 70;  
RESULT 1416  
ID ABB99751 standard; protein; 327 AA.  
DE Amino acid sequence of bacteriophage phiCm1 antigenic protein.  
PN WO200295413-A2.  
PD 28-NOV-2002.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
Query Match 5.7%; Score 68.5; DB 6; Length 327;



Best Local Similarity 27.0%; Pred. No. 71;  
RESULT 1417  
ID AAW25926 standard; protein; 354 AA.  
DE Xenopus-melatonin receptor MEL-1A.  
PN WO9704094-A1.  
PD 06-FEB-1997.  
PA (ADIR ) ADIR & CIE.  
Query Match 5.7%; Score 68.5; DB 2; Length 354;  
Best Local Similarity 18.8%; Pred. No. 79;  
RESULT 1418  
ID AAY87506 standard; protein; 369 AA.  
DE Human G coupled-protein receptor, GPR10.  
PN WO20017641-A1.  
PD 30-MAR-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 5.7%; Score 68.5; DB 3; Length 369;  
Best Local Similarity 23.3%; Pred. No. 84;  
RESULT 1419  
ID AAE13430 standard; protein; 377 AA.  
DE Brascica napus microsomal omega-3 desaturase, bnfAD3 protein.  
PN WO200179499-A1.  
PD 25-OCT-2001.  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
Query Match 5.7%; Score 68.5; DB 4; Length 377;  
Best Local Similarity 29.3%; Pred. No. 87;  
RESULT 1420  
ID AAB28521 standard; protein; 382 AA.  
DE Mouse Edg1 polypeptide.  
PN WO200059529-A1.  
PD 12-OCT-2000.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 5.7%; Score 68.5; DB 3; Length 382;  
Best Local Similarity 19.8%; Pred. No. 88;  
RESULT 1421  
ID AAM85456 standard; protein; 382 AA.  
DE Mouse protein sequence mcp20760.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 5.7%; Score 68.5; DB 7; Length 382;  
Best Local Similarity 19.8%; Pred. No. 88;  
RESULT 1422  
ID ADO29286 standard; protein; 382 AA.  
DE Mouse GPCR EDG1, SEQ ID NO:387.  
PN WO200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 382;  
Best Local Similarity 19.8%; Pred. No. 88;  
RESULT 1423  
ID ADR67019 standard; protein; 382 AA.  
DE Mouse cancer associated protein sequence SEQ ID NO:65.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 382;  
Best Local Similarity 19.8%; Pred. No. 88;  
RESULT 1424  
ID AAM01664 standard; protein; 383 AA.  
DE P(rat-edg), G-protein coupled receptor.  
PN US5585476-A.  
PD 17-DEC-1996.  
PA (MACL/) MACLENNAN A J.  
Query Match 5.7%; Score 68.5; DB 2; Length 383;  
Best Local Similarity 19.8%; Pred. No. 89;  
RESULT 1425  
ID AAM87791 standard; protein; 383 AA.  
DE Rat-edg, G-protein coupled receptor superfamily member.  
PN US5585443-A.  
PD 05-JAN-1999.  
PA (MACL/) MACLENNAN A J.  
Query Match 5.7%; Score 68.5; DB 2; Length 383;  
Best Local Similarity 19.8%; Pred. No. 89;

RESULT 1426  
ID ABU61817 standard; protein; 383 AA.  
DE Rat-edg.  
PN US6518414-B1.  
PD 11-FEB-2003.  
PA (MACL/) MACLENNAN A J.  
Query Match 5.7%; Score 68.5; DB 7; Length 383;  
Best Local Similarity 19.8%; Pred. No. 89;  
RESULT 1427  
ID ABG07020 standard; protein; 404 AA.  
DE Novel human diagnostic protein #7011.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.7%; Score 68.5; DB 4; Length 404;  
Best Local Similarity 22.4%; Pred. No. 95;  
RESULT 1428  
ID AAB68619 standard; protein; 411 AA.  
DE Human PAC\_1 receptor isoform 30.  
PN WO200107478-A1.  
PD 01-FEB-2001.  
PA (MEDI-) MEDICAL RES COUNCIL.  
Query Match 5.7%; Score 68.5; DB 4; Length 411;  
Best Local Similarity 29.9%; Pred. No. 98;  
RESULT 1429  
ID ADH87117 standard; protein; 417 AA.  
DE Enterococcus faecalis polypeptide #1597.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 5.7%; Score 68.5; DB 7; Length 417;  
Best Local Similarity 23.2%; Pred. No. 1e+02;  
RESULT 1430  
ID AAB88409 standard; protein; 420 AA.  
DE High-affinity melatonin receptor.  
PN WO9535320-A1.  
PD 28-DEC-1995.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
Query Match 5.7%; Score 68.5; DB 2; Length 420;  
Best Local Similarity 18.8%; Pred. No. 1e+02;  
RESULT 1431  
ID AAM88344 standard; protein; 430 AA.  
DE Salmonella enterica O antigen pathway flippase protein.  
PN WO9850531-A1.  
PD 12-NOV-1998.  
PA (UNSY ) UNIV SYDNEY.  
Query Match 5.7%; Score 68.5; DB 2; Length 430;  
Best Local Similarity 23.6%; Pred. No. 1e+02;  
RESULT 1432  
ID AAU02941 standard; protein; 431 AA.  
DE Angiotensin converting enzyme (ACEV) splice variant protein #41.  
PN WO200136632-A2.  
PD 25-MAY-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 5.7%; Score 68.5; DB 4; Length 431;  
Best Local Similarity 29.9%; Pred. No. 1e+02;  
RESULT 1433  
ID ADA33815 standard; protein; 437 AA.  
DE Actinobacter baumannii protein #976.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 68.5; DB 6; Length 437;  
Best Local Similarity 20.5%; Pred. No. 1.1e+02;  
RESULT 1434  
ID ADS12084 standard; protein; 443 AA.  
DE Human therapeutic contig protein - SEQ ID 2321.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 443;  
Best Local Similarity 19.6%; Pred. No. 1.1e+02;

RESULT 1435  
ID AAB7186 standard; protein; 444 AA.  
DE Human CRP seven transmembrane domain.  
PN WO200109328-A1.  
PD 08-FEB-2001.  
PA (MIL-) MILLENNIUM PHARM INC.  
Query Match 5.7%; Score 68.5; DB 4; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1436  
ID AAE26685 standard; protein; 444 AA.  
DE Human CRP-R2 splice variant protein.  
PN US202055617-A1.  
PD 09-MAY-2002.  
PA (PERR/) PERRIN M. H.  
PA (CHEN/) CHEN R.  
PA (LEW/) LEWIS K. A.  
PA (VALE/) VALE W. W.  
PA (DONA/) DONALDSON C. J.  
PA (SAMC/) SAMCHENKO P.  
Query Match 5.7%; Score 68.5; DB 5; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1437  
ID ABR43052 standard; protein; 444 AA.  
DE Human CRP-R1 beta chain.  
PN WO2003024990-A2.  
PD 27-MAR-2003.  
PA (UYTE-) UNIV TENNESSEE RES CORP.  
Query Match 5.7%; Score 68.5; DB 6; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1438  
ID ABU08081 standard; protein; 444 AA.  
DE Human corticotropin-releasing factor receptor 2 (CRF-R2).  
PN US6495343-B1.  
PD 17-DEC-2002.  
PA (SALK-) SALK INST BIOLOGICAL STUDIES.  
Query Match 5.7%; Score 68.5; DB 6; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1439  
ID ABG76402 standard; protein; 444 AA.  
DE Human hCRP-R1, splice variant.  
PN US6482608-B1.  
PD 19-NOV-2002.  
PA (SALK-) SALK INST BIOLOGICAL STUDIES.  
Query Match 5.7%; Score 68.5; DB 6; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1440  
ID ADE62734 standard; protein; 444 AA.  
DE Human Protein p34998, SEQ ID NO 8667.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 5.7%; Score 68.5; DB 7; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1441  
ID ADU65810 standard; protein; 444 AA.  
DE Human corticotropin-releasing factor receptor CRF-RA2.  
PN US2004035173-A1.  
PD 26-FEB-2004.  
PA (SALK-) SALK INST BIOLOGICAL STUDIES.  
Query Match 5.7%; Score 68.5; DB 8; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1442  
ID ADC86255 standard; protein; 447 AA.  
DE Human GPCR protein SEQ ID NO:708.  
PN EPI270724-A2.  
PD 02-JAN-2003.  
PA (NAD-) NAT INST ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 5.7%; Score 68.5; DB 7; Length 447;  
Best Local Similarity 23.7%; Pred. No. 1.1e+02;  
RESULT 1443  
ID AAR58668 standard; protein; 448 AA.

DE Human PACAP receptor type 1A mature protein.  
PN EPI18291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.7%; Score 68.5; DB 2; Length 448;  
Best Local Similarity 29.9%; Pred. No. 1.1e+02;  
RESULT 1444  
ID ABB56380 standard; protein; 468 AA.  
DE Non-endogenous human GPCR protein, SEQ ID NO: 553.  
PN WO20017172-A2.  
PD 18-OCT-2001.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.7%; Score 68.5; DB 4; Length 468;  
Best Local Similarity 29.9%; Pred. No. 1.2e+02;  
RESULT 1445  
ID AAB71874 standard; protein; 468 AA.  
DE Human PACR seven transmembrane domain.  
PN WO200109328-A1.  
PD 08-FEB-2001.  
PA (MIL-) MILLENNIUM PHARM INC.  
Query Match 5.7%; Score 68.5; DB 4; Length 468;  
Best Local Similarity 29.9%; Pred. No. 1.2e+02;  
RESULT 1446  
ID ADC86185 standard; protein; 468 AA.  
DE Human GPCR protein SEQ ID NO:638.  
PN EPI270724-A2.  
PD 02-JAN-2003.  
PA (NAD-) NAT INST ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 5.7%; Score 68.5; DB 7; Length 468;  
Best Local Similarity 29.9%; Pred. No. 1.2e+02;  
RESULT 1447  
ID ADO29153 standard; protein; 468 AA.  
DE Human GPCR ADCTAP1R1, SEQ ID NO:254.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 468;  
Best Local Similarity 29.9%; Pred. No. 1.2e+02;  
RESULT 1448  
ID AAR58670 standard; protein; 475 AA.  
DE Human PACAP receptor type 1-B2 mature protein.  
PN EPI18291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.7%; Score 68.5; DB 2; Length 475;  
Best Local Similarity 29.9%; Pred. No. 1.2e+02;  
RESULT 1449  
ID AAR58671 standard; protein; 476 AA.  
DE Human PACAP receptor type 1C mature protein.  
PN EPI18291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.7%; Score 68.5; DB 2; Length 476;  
Best Local Similarity 29.9%; Pred. No. 1.2e+02;  
RESULT 1450  
ID AAR58669 standard; protein; 476 AA.  
DE Human PACAP receptor type 1B mature protein.  
PN EPI18291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.7%; Score 68.5; DB 2; Length 476;  
Best Local Similarity 29.9%; Pred. No. 1.2e+02;  
RESULT 1451  
ID ADN24160 standard; protein; 488 AA.  
DE Bacterial polypeptide #6813.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G. J.  
PA (SLAT/) SLATER S. C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B. S.

Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 8; Length 488;  
RESULT 1452  
ID AAB65829 standard; protein; 495 AA.  
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:573.  
PN EP127152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 495;  
RESULT 1453  
ID AAB68618 standard; protein; 524 AA.  
DE Human PAC 1 receptor.  
PN WO200107478-A1.  
PD 01-FEB-2001.  
PA (MEDI-) MEDICAL RES COUNCIL.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 4; Length 524;  
RESULT 1454  
ID AAR58659 standard; protein; 525 AA.  
DE Human PACAP receptor type 1A protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKA ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 2; Length 525;  
RESULT 1455  
ID ABH08611 standard; protein; 525 AA.  
DE Human pituitary adenylate cyclase (PAC) 1 receptor.  
PN US2002182729-A1.  
PD 05-DEC-2002.  
PA (DICI/) DICICCO-BLOOM E.  
PA (NICO/) NICOT A.  
PA (LUNN/) LU N.  
PA (SUHJ/) SUH J.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 6; Length 525;  
RESULT 1456  
ID ABB91873 standard; protein; 525 AA.  
DE Human PACAP receptor type 1 protein SEQ ID NO:231.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 6; Length 525;  
RESULT 1457  
ID ADN38958 standard; protein; 525 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:276.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 7; Length 525;  
RESULT 1458  
ID ABB73995 standard; protein; 541 AA.  
DE Candida albicans essential protein SEQ ID NO 7832.  
PN WO200253728-A2.  
PD 11-JUL-2002.  
PA (BLIT-) BLITTA PHARM INC.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 541;  
RESULT 1459  
ID ABG95329 standard; protein; 548 AA.  
DE Human novel secreted protein #150.  
PN US6420526-B1.  
PD 16-JUL-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 548;  
RESULT 1460  
ID ABO34523 standard; protein; 548 AA.  
DE Region of human secreted protein encoded by cDNA sequence #150.  
PN US2003049618-A1.

PD 13-MAR-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FER/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJ/) HU J.  
PA (FLO/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAF/) LAFLEUR D W.  
PA (LITY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 6; Length 548;  
RESULT 1461  
ID AD123184 standard; protein; 548 AA.  
DE Novel human secreted protein seq id 469.  
PN US2003175858-A1.  
PD 18-SEP-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (SOP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D P.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FER/) FERRIE A M.  
PA (DUAN/) DUAN D R.  
PA (HUJ/) HU J.  
PA (FLO/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (FISC/) FISCHER C L.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAF/) LAFLEUR D W.  
PA (LITY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (KYAW/) KYAW H.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 7; Length 548;  
RESULT 1462  
ID ADH17089 standard; protein; 548 AA.  
DE Human translaton inflation factor eIF3 p66 subunit protein.  
PN WO2003097854-A2.  
PD 27-NOV-2003.  
PA (SUGB-) SUGEN INC.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 8; Length 548;  
RESULT 1463  
ID ADH74186 standard; protein; 548 AA.  
DE Human secreted protein #150.  
PN US2003225246-A1.  
PD 04-DEC-2003.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 548;  
Best Local Similarity 34.0%; Pred. No. 1.5e+02;  
RESULT 1464  
ID ASM82346 standard; protein; 548 AA.  
DE Tumour-associated antigenic target (TAR) polypeptide PRO22481, SEQ:6028.  
PN W02004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 548;  
Best Local Similarity 34.0%; Pred. No. 1.5e+02;  
RESULT 1465  
ID AAR58661 standard; protein; 552 AA.  
DE Human PACAP receptor type 1-B2 protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE) TAKEEDA CHEM IND LTD.  
Query Match 5.7%; Score 68.5; DB 2; Length 552;  
Best Local Similarity 29.9%; Pred. No. 1.5e+02;  
RESULT 1466  
ID AAR58662 standard; protein; 553 AA.  
DE Human PACAP receptor type 1C protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE) TAKEEDA CHEM IND LTD.  
Query Match 5.7%; Score 68.5; DB 2; Length 553;  
Best Local Similarity 29.9%; Pred. No. 1.5e+02;  
RESULT 1467  
ID AAR58660 standard; protein; 553 AA.  
DE Human PACAP receptor type 1B protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE) TAKEEDA CHEM IND LTD.  
Query Match 5.7%; Score 68.5; DB 2; Length 553;  
Best Local Similarity 29.9%; Pred. No. 1.5e+02;  
RESULT 1468  
ID ABB11705 standard; peptide; 588 AA.  
DE Human GABA transporter homologue, SEQ ID NO:2075.  
PN W0200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.7%; Score 68.5; DB 4; Length 588;  
Best Local Similarity 19.6%; Pred. No. 1.6e+02;  
RESULT 1469  
ID ADP9892 standard; protein; 597 AA.  
DE C. albicans specific gene, orf6.4254, protein sequence.  
PN W02004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 597;  
Best Local Similarity 26.2%; Pred. No. 1.6e+02;  
RESULT 1470  
ID ADS10834 standard; protein; 600 AA.  
DE Human therapeutic protein - SEQ ID 1071.  
PN W02004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 5.7%; Score 68.5; DB 8; Length 600;  
Best Local Similarity 19.6%; Pred. No. 1.6e+02;  
RESULT 1471  
ID ABB38306 standard; protein; 634 AA.  
DE Protein encoded by Prokaryotic essential gene #28333.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.7%; Score 68.5; DB 6; Length 634;  
Best Local Similarity 26.3%; Pred. No. 1.8e+02;  
RESULT 1472  
ID ABO81139 standard; protein; 660 AA.  
DE Pseudomonas aeruginosa polypeptide #13314.  
PN US6551795-B1.  
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 68.5; DB 7; Length 660;  
Best Local Similarity 26.3%; Pred. No. 1.9e+02;  
RESULT 1473  
ID AAG20246 standard; protein; 663 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22359.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 68.5; DB 3; Length 663;  
Best Local Similarity 22.3%; Pred. No. 1.9e+02;  
RESULT 1474  
ID ABB53933 standard; protein; 670 AA.  
DE Lactococcus lactis protein kxp1.  
PN PR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 5.7%; Score 68.5; DB 5; Length 670;  
Best Local Similarity 22.1%; Pred. No. 1.9e+02;  
RESULT 1475  
ID ABB50927 standard; protein; 691 AA.  
DE Helicobacter pylori selected interacting domain (SID) protein #270.  
PN W0200266501-A2.  
PD 29-AUG-2002.  
PA (HYBR-) HYBRIGENICS.  
PA (INSP) INST PASTEUR.  
Query Match 5.7%; Score 68.5; DB 5; Length 691;  
Best Local Similarity 19.2%; Pred. No. 2e+02;  
RESULT 1476  
ID AAG20245 standard; protein; 704 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22358.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 68.5; DB 3; Length 704;  
Best Local Similarity 22.3%; Pred. No. 2.1e+02;  
RESULT 1477  
ID AAG20244 standard; protein; 724 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22357.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 68.5; DB 3; Length 724;  
Best Local Similarity 22.3%; Pred. No. 2.1e+02;  
RESULT 1478  
ID AAU72535 standard; protein; 724 AA.  
DE Arabidopsis cell cycle protein CCP25.  
PN W0200185946-A2.  
PD 15-NOV-2001.  
PA (CROP-) CROPDISEIGN NV.  
Query Match 5.7%; Score 68.5; DB 5; Length 724;  
Best Local Similarity 22.3%; Pred. No. 2.1e+02;  
RESULT 1479  
ID ADS23914 standard; protein; 731 AA.  
DE Bacterial polypeptide #12947.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 5.7%; Score 68.5; DB 8; Length 731;  
Best Local Similarity 25.9%; Pred. No. 2.2e+02;  
RESULT 1480  
ID ADC95469 standard; protein; 738 AA.  
DE E. faecium protein sequence SEQ ID 5096.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.7%; Score 68.5; DB 7; Length 738;  
Best Local Similarity 20.3%; Pred. No. 2.2e+02;  
RESULT 1481  
ID AAB46310 standard; protein; 788 AA.  
DE H. pylori Hps115 protein.  
PN W0200073502-A2.

PD 07-DEC-2000.  
PA (PLAC-) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.  
PA (CREA-) CREATOGEN GMBH.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 4; Length 788;  
RESULT 1482  
ID AAY92103 standard; protein; 885 AA.  
DE Human WFS1 mutant DEL508 YYLL.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 885;  
RESULT 1483  
ID AAY92105 standard; protein; 890 AA.  
DE Human WFS1 mutant G695V.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 890;  
RESULT 1484  
ID AAY92107 standard; protein; 890 AA.  
DE Human WFS1 mutant F504L.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 890;  
RESULT 1485  
ID AAY92110 standard; protein; 890 AA.  
DE Human WFS1 polymorphism I333V.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 890;  
RESULT 1486  
ID AAY92109 standard; protein; 890 AA.  
DE Human WFS1 polymorphism R456H.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 890;  
RESULT 1487  
ID AAY92100 standard; protein; 890 AA.  
DE WFS1 polypeptide.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 890;  
RESULT 1488  
ID AAY92104 standard; protein; 890 AA.

DE Human WFS1 mutant P724L.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 890;  
RESULT 1489  
ID AAB29861 standard; protein; 894 AA.  
DE Streptococcus polypeptide SEQ ID NO 8898.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 894;  
RESULT 1490  
ID AAB28153 standard; protein; 894 AA.  
DE Streptococcus polypeptide SEQ ID NO 5482.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 894;  
RESULT 1491  
ID AAY92102 standard; protein; 937 AA.  
DE Human WFS1 mutant del1882fs/ter937.  
PN WO200018787-A1.  
PD 06-APR-2000.  
PA (UNITW) UNIV WASHINGTON.  
PA (PERM/) PERMUTT M A.  
PA (INOU/) INOUE H.  
PA (MUEC/) MUECKLER M.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 3; Length 937;  
RESULT 1492  
ID ADN19015 standard; protein; 1004 AA.  
DE Bacterial polypeptide #1668.  
PN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 8; Length 1004;  
RESULT 1493  
ID ADB70303 standard; protein; 1178 AA.  
DE C. neoformans amino acid sequence SEQ ID NO:3347.  
PN WO2003052076-A2.  
PD 26-JUN-2003.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 7; Length 1178;  
RESULT 1494  
ID AAM88448 standard; protein; 1296 AA.  
DE Caenorhabditis elegans NPCL protein orthologue.  
PN WO9901555-A1.  
PD 14-JAN-1999.  
PA (USSH) US DEPT HEALTH & HUMAN RESOURCES.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 2; Length 1296;  
RESULT 1495  
ID AAB30730 standard; protein; 3015 AA.  
DE Amino acid sequence of chimeric Hepatitis C virus clone pH77CV-J6S.  
PN WO200075338-A2.  
PD 14-DEC-2000.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match  
Best Local Similarity 5.7%; Score 68.5; DB 4; Length 3015;

Best Local Similarity 26.7%; Pred. No. 1.5e+03;  
RESULT 1496  
ID AAB30732 standard; protein; 3015 AA.  
DE Amino acid sequence of chimeric Hepatitis C virus clone J6S.  
PN WO200075338-A2.  
PD 14-DEC-2000.  
PA (US9H ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.7%; Score 68.5; DB 4; Length 3015;  
Best Local Similarity 26.7%; Pred. No. 1.5e+03;  
RESULT 1497  
ID ADK16845 standard; protein; 200 AA.  
DE Nanorarchaeum equitans cancer-associated (CA) protein #398.  
PN WO2003093434-A2.  
PD 13-NOV-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 5.7%; Score 68; DB 8; Length 200;  
Best Local Similarity 23.5%; Pred. No. 41;  
RESULT 1498  
ID AAB78946 standard; protein; 247 AA.  
DE C. glutamicum SRT protein sequence SEQ ID NO:152.  
PN WO200100804-A2.  
PD 04-JAN-2001.  
PA (BADI ) BASF AG.  
Query Match 5.7%; Score 68; DB 4; Length 247;  
Best Local Similarity 23.1%; Pred. No. 55;  
RESULT 1499  
ID AAG91355 standard; protein; 247 AA.  
DE C glutamicum protein fragment SEQ ID NO: 5109.  
PN EP108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 5.7%; Score 68; DB 4; Length 247;  
Best Local Similarity 23.1%; Pred. No. 55;  
RESULT 1500  
ID AAY41212 standard; protein; 258 AA.  
DE E. coli MCB polypeptide.  
PN WO9951753-A1.  
PD 14-OCT-1999.  
PA (UTAL-) UNITIV ALBERTA.  
Query Match 5.7%; Score 68; DB 2; Length 258;  
Best Local Similarity 23.0%; Pred. No. 59;

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OM protein - protein search, using bw model

Run on: May 17, 2005, 10:22:46 ; Search time 138 Seconds  
(without alignments)  
566.436 Million cell updates/sec

Perfect score: 1195  
Sequence: 1 NMHLPEDMENALTGSSQSHA.....EAGSEAEKQDSKDLLEL 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :

- 1: /cgn2\_6/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/2/pubppaa/PCF\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/2/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/2/pubppaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/2/pubppaa/PCFUS\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/2/pubppaa/US08\_NEW\_PUB.pep:\*
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- 8: /cgn2\_6/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
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- 19: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep:\*
- 20: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
449	1195	100.0	234	14	US-10-223-085-62
446	1195	100.0	234	14	US-10-223-084-62
467	1195	100.0	234	14	US-10-223-086-62
468	1195	100.0	234	14	US-10-223-090-62
470	1195	100.0	234	14	US-10-223-087-62
478	1195	100.0	234	14	US-10-223-083-62
481	1195	100.0	234	14	US-10-223-089-62
498	1195	100.0	234	14	US-10-174-587-66
562	1195	100.0	234	14	US-10-063-742-14
640	1195	100.0	234	14	US-10-223-081-62
650	1195	100.0	234	14	US-10-223-082-62
665	1195	100.0	234	14	US-10-144-194A-20
670	1195	100.0	234	15	US-10-305-654-62
675	1195	100.0	234	15	US-10-081-056-62

681	1195	100.0	234	17	US-10-972-317-14	Sequence 14, Appl
682	1188	99.4	234	15	US-10-262-839-84	Sequence 84, Appl
683	1024	85.7	201	15	US-10-264-237-2663	Sequence 2663, Ap
684	985	82.4	198	15	US-10-262-839-82	Sequence 82, Appl
685	669.5	56.0	146	15	US-10-104-047-2567	Sequence 2567, Ap
686	56.6	44.5	145	15	US-10-174-293-236	Sequence 296, App
687	664	55.6	445	15	US-10-435-696-33	Sequence 33, Appl
688	578	48.4	412	17	US-10-491-213-22	Sequence 22, Appl
689	91	7.6	373	14	US-10-091-007-198	Sequence 198, App
690	90.5	7.6	803	16	US-10-437-963-136814	Sequence 136814,
691	87.5	7.3	516	9	US-09-925-298-653	Sequence 653, App
692	87.5	7.3	516	14	US-10-102-806-653	Sequence 653, App
693	87	7.3	421	17	US-10-741-600-929	Sequence 929, App
694	85.5	7.2	223	17	US-10-741-600-926	Sequence 926, App
695	85.5	7.2	285	17	US-10-741-600-921	Sequence 921, App
696	85.5	7.2	315	17	US-10-741-600-925	Sequence 925, App
697	85.5	7.2	323	17	US-10-741-600-923	Sequence 923, App
698	85.5	7.2	328	17	US-10-741-600-924	Sequence 924, App
699	85.5	7.2	338	17	US-10-741-600-928	Sequence 928, App
700	85.5	7.2	339	17	US-10-741-600-930	Sequence 930, App
701	85.5	7.2	384	17	US-10-741-600-932	Sequence 932, App
702	85.5	7.2	390	17	US-10-741-600-927	Sequence 927, App
703	85.5	7.2	396	15	US-10-282-122A-34604	Sequence 54604, A
704	85.5	7.2	438	17	US-10-741-600-931	Sequence 931, App
705	85.5	7.2	440	15	US-10-262-511-182	Sequence 182, App
706	85.5	7.2	473	15	US-10-264-237-2016	Sequence 2016, Ap
707	85.5	7.2	500	15	US-10-282-122A-68468	Sequence 68468, A
708	85	7.1	527	15	US-10-425-114-65247	Sequence 65247, A
709	85	7.1	797	14	US-10-156-761-11433	Sequence 11433, A
710	84.5	7.1	430	15	US-10-282-122A-61134	Sequence 61134, A
711	84.5	6.9	886	16	US-10-437-963-11543	Sequence 11543,
712	82.5	6.9	239	15	US-10-282-122A-63532	Sequence 63532, A
713	82.5	6.9	341	14	US-10-216-209-92	Sequence 92, Appl
714	82	6.8	359	14	US-10-205-194-144	Sequence 144, App
715	81.5	6.8	284	15	US-10-425-114-44166	Sequence 44166, A
716	81.5	6.8	436	15	US-10-424-599-272132	Sequence 272132,
717	81.5	6.8	659	16	US-10-437-963-128426	Sequence 128426,
718	81	6.8	529	15	US-10-369-499-5808	Sequence 5808, Ap
719	81	6.8	529	15	US-10-369-499-5808	Sequence 5808, Ap
720	80.5	6.7	433	15	US-10-282-122A-60960	Sequence 60960, A
721	80.5	6.7	463	15	US-10-282-122A-60960	Sequence 60960, A
722	80	6.7	891	14	US-10-925-297-851	Sequence 851, Appl
723	80	6.7	144	9	US-09-925-297-851	Sequence 851, Appl
724	80	6.7	238	15	US-10-108-260A-3158	Sequence 3158, Ap
725	80	6.7	360	11	US-09-833-245-1308	Sequence 1308, Ap
726	80	6.7	536	15	US-10-425-114-37103	Sequence 37103, A
727	80	6.7	531	15	US-10-424-599-169136	Sequence 169136,
728	79.5	6.7	355	15	US-10-282-122A-33478	Sequence 53478, A
729	79.5	6.7	406	14	US-10-223-538-4	Sequence 4, Appl1
730	79	6.6	723	15	US-10-257-023-4	Sequence 4, Appl1
731	79	6.6	121	15	US-10-335-977-8880	Sequence 8880, Ap
732	79	6.6	1531	15	US-10-353-699-110	Sequence 110, App
733	78.5	6.6	1597	9	US-09-832-892-35	Sequence 35, Appl
734	78.5	6.6	135	14	US-10-029-386-29323	Sequence 29323, A
735	78.5	6.6	239	15	US-10-282-122A-64222	Sequence 64222, A
736	78.5	6.6	766	9	US-09-795-693-17	Sequence 17, Appl
737	78.5	6.6	766	13	US-10-072-621-6	Sequence 6, Appl1
738	78.5	6.6	766	14	US-10-156-239-17	Sequence 17, Appl
739	78.5	6.6	766	14	US-10-159-485-17	Sequence 17, Appl
740	78	6.5	355	9	US-09-938-719-9	Sequence 9, Appl1
741	78	6.5	355	9	US-09-938-703-9	Sequence 9, Appl1
742	78	6.5	355	16	US-10-661-798-9	Sequence 9, Appl1
743	78	6.5	355	16	US-10-661-798-9	Sequence 9, Appl1
744	78	6.5	411	9	US-09-815-442-11138	Sequence 11138, A
745	77.5	6.5	471	15	US-10-282-122A-58335	Sequence 58335, A
746	77.5	6.5	280	15	US-10-243-552-905	Sequence 905, App
747	77.5	6.5	337	15	US-10-282-122A-16813	Sequence 16813, A
748	77.5	6.5	398	16	US-10-437-963-153107	Sequence 153107,
749	77.5	6.5	491	15	US-10-369-499-21395	Sequence 21395, A
750	77.5	6.5	892	15	US-10-437-963-195051	Sequence 195051, A
751	77.5	6.5	892	14	US-10-226-629A-15	Sequence 15, Appl
752	77	6.4	630	15	US-10-282-122A-44096	Sequence 44096, A
753	77	6.4	735	16	US-10-437-963-162148	Sequence 162148,



754	77	6.4	1391	16	US-10-437-963-128235	Sequence 128235,	827	73	6.1	354	14	US-10-303-204A-16	Sequence 16, Appl
755	76.5	6.4	453	13	US-10-437-963-156098	Sequence 156098,	828	73	6.1	377	9	US-09-939-980-533	Sequence 533, Appl
756	76.5	6.4	494	16	US-10-143-002-4	Sequence 4, Appl1	829	73	6.1	450	16	US-10-626-830-59	Sequence 59, Appl1
757	76.5	6.4	494	14	US-10-325-891-4	Sequence 4, Appl1	830	73	6.1	453	15	US-10-282-122A-59343	Sequence 59343, A
758	76.5	6.4	555	15	US-10-104-047-2011	Sequence 2011, Ap	831	73	6.1	526	15	US-10-038-856-30	Sequence 30, Appl
759	76.5	6.4	570	15	US-10-415-187-3	Sequence 3, Appl1	832	73	6.1	553	15	US-10-282-122A-59060	Sequence 59060, A
760	76.5	6.4	589	15	US-10-335-977-6022	Sequence 6022, Ap	833	73	6.1	635	16	US-10-788-792-140	Sequence 140, Appl
761	76.5	6.4	593	15	US-10-335-977-6023	Sequence 6023, Ap	834	73	6.1	748	9	US-09-815-242-12792	Sequence 12792, A
762	76.5	6.4	638	15	US-10-424-599-214477	Sequence 214477,	835	73	6.1	750	10	US-09-746-788-86	Sequence 86, Appl1
763	76.5	6.4	2539	15	US-10-369-493-3779	Sequence 3779, Ap	836	73	6.1	788	15	US-10-282-122A-70316	Sequence 70316, A
764	76	6.4	295	15	US-10-424-599-163113	Sequence 163113,	837	73	6.1	792	17	US-09-815-242-12327	Sequence 12327, A
765	76	6.4	456	15	US-10-264-237-1800	Sequence 1800, Ap	838	73	6.1	792	17	US-10-470-048B-334	Sequence 334, App
766	76	6.4	456	9	US-09-925-299-940	Sequence 940, App	839	73	6.1	806	16	US-10-437-963-173527	Sequence 173527,
767	76	6.4	557	10	US-09-925-299-940	Sequence 940, App	840	73	6.1	966	9	US-09-828-466-6	Sequence 6, Appl1
768	76	6.4	1402	15	US-10-369-493-5502	Sequence 5502, App	841	73	6.1	971	16	US-10-788-792-141	Sequence 141, Appl
769	76	6.4	1917	15	US-10-369-493-6036	Sequence 6036, Ap	842	73	6.1	971	17	US-10-624-727-49	Sequence 49, Appl
770	75.5	6.3	129	15	US-10-424-599-266695	Sequence 266695,	843	73	6.1	971	17	US-10-624-727-49	Sequence 59, Appl
771	75.5	6.3	253	16	US-10-437-963-188833	Sequence 188833,	844	72.5	6.1	209	14	US-10-080-170-107	Sequence 107, App
772	75.5	6.3	263	10	US-09-769-787-119	Sequence 119, App	845	72.5	6.1	209	16	US-10-080-170-107	Sequence 107, App
773	75.5	6.3	263	10	US-09-769-787-119	Sequence 3518, Ap	846	72.5	6.1	209	16	US-10-468-356-107	Sequence 107, App
774	75.5	6.3	276	17	US-10-451-467A-528	Sequence 528, App	847	72.5	6.1	222	15	US-10-282-122A-43226	Sequence 43226, A
775	75.5	6.3	352	9	US-09-912-020-293	Sequence 293, App	848	72.5	6.1	222	15	US-10-424-599-205057	Sequence 205057,
776	75.5	6.3	463	15	US-10-369-493-13372	Sequence 13372, A	849	72.5	6.1	274	15	US-10-425-114-58050	Sequence 58050, A
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778	75	6.3	473	16	US-10-004-378A-104	Sequence 104, App	851	72.5	6.1	279	15	US-10-424-599-187241	Sequence 187241,
779	75	6.3	473	16	US-10-755-889-598	Sequence 598, App	852	72.5	6.1	279	15	US-10-424-599-187241	Sequence 163110,
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781	75	6.3	789	16	US-10-437-963-188379	Sequence 188379,	854	72.5	6.1	307	15	US-10-425-114-66808	Sequence 66808, A
782	75	6.3	874	16	US-10-437-963-153160	Sequence 153160,	855	72.5	6.1	307	15	US-10-425-114-67080	Sequence 66829, A
783	75	6.3	1131	15	US-10-104-047-2866	Sequence 2866, Ap	856	72.5	6.1	308	15	US-10-425-114-66829	Sequence 66829, A
784	74.5	6.2	263	16	US-10-437-963-149181	Sequence 149181,	857	72.5	6.1	310	15	US-10-425-114-66745	Sequence 66745, A
785	74.5	6.2	355	9	US-09-789-482-4	Sequence 4, Appl1	858	72.5	6.1	310	15	US-10-425-114-66745	Sequence 66745, A
786	74.5	6.2	355	9	US-09-789-486-4	Sequence 4, Appl1	859	72.5	6.1	311	15	US-10-425-114-65277	Sequence 65277, A
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788	74.5	6.2	355	14	US-10-251-385-130	Sequence 130, App	861	72.5	6.1	312	15	US-10-425-114-66930	Sequence 66930, A
789	74.5	6.2	355	14	US-10-225-567A-249	Sequence 249, App	862	72.5	6.1	389	15	US-10-350-924-1	Sequence 215, App
790	74.5	6.2	355	14	US-10-239-423-82	Sequence 367, App	863	72.5	6.1	389	15	US-10-350-924-1	Sequence 1, Appl1
791	74.5	6.2	355	14	US-10-741-601-367	Sequence 367, App	864	72.5	6.1	448	9	US-09-935-371-16	Sequence 16, Appl
792	74.5	6.2	355	16	US-10-741-601-367	Sequence 1084, Ap	865	72.5	6.1	448	9	US-09-935-371-16	Sequence 14, Appl
793	74.5	6.2	355	16	US-10-741-601-368	Sequence 368, App	866	72.5	6.1	448	9	US-09-935-371-16	Sequence 17, Appl
794	74.5	6.2	362	17	US-10-741-600-1085	Sequence 1085, Ap	867	72.5	6.1	513	9	US-09-935-371-15	Sequence 15, Appl
795	74.5	6.2	471	6	US-09-929-513-4	Sequence 4, Appl1	868	72.5	6.1	522	15	US-10-369-499-2418	Sequence 2418, Ap
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797	74.5	6.2	661	15	US-10-425-114-37283	Sequence 37283, A	870	72.5	6.1	621	15	US-10-424-599-229567	Sequence 90, Appl
798	74.5	6.2	3010	16	US-10-333-449A-34	Sequence 34, Appl	871	72.5	6.1	848	9	US-09-882-986-2	Sequence 2, Appl1
799	74.5	6.2	301	15	US-10-424-599-268067	Sequence 268067,	872	72.5	6.1	848	15	US-10-425-114-65959	Sequence 53063, A
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803	74	6.2	350	14	US-10-112-356-7	Sequence 7, Appl1	876	72	6.0	123	16	US-10-437-963-154005	Sequence 154005,
804	74	6.2	350	14	US-10-225-567A-164	Sequence 164, App	877	72	6.0	224	14	US-10-017-163-570	Sequence 570, App
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808	73.5	6.2	192	10	US-09-791-932-85	Sequence 85, Appl1	881	72	6.0	334	9	US-09-925-299-932	Sequence 932, App
809	73.5	6.2	208	16	US-10-767-701-46027	Sequence 46027, A	882	72	6.0	335	15	US-10-424-599-144842	Sequence 148442,
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818	73	6.1	114	15	US-10-335-977-8879	Sequence 8879, Ap	891	72	6.0	656	14	US-10-241-220-83	Sequence 84, Appl
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820	73	6.1	255	5	US-10-335-977-5926	Sequence 5926, Ap	893	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl
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824	73	6.1	272	15	US-10-912-446-75	Sequence 75, Appl	897	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl
825	73	6.1	276	17	US-10-335-977-5928	Sequence 5928, App	898	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl
826	73	6.1	342	14	US-10-177-293-160	Sequence 160, App	899	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl

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909	71.5	6.0	353	16	US-10-262-313-8	Sequence 8, Appl1	982	71	5.9	777	15	US-10-114-270-190	Sequence 190, App
910	71.5	6.0	363	16	US-10-768-878-8	Sequence 8, Appl1	983	71	5.9	788	15	US-10-335-977-5540	Sequence 5540, Ap
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915	71.5	6.0	382	10	US-09-504-099-1	Sequence 1, Appl1	988	70.5	5.9	218	14	US-10-115-577A-64	Sequence 64, Appl
916	71.5	6.0	382	13	US-10-087-192-786	Sequence 786, App	989	70.5	5.9	228	13	US-10-051-902-16	Sequence 16, Appl1
917	71.5	6.0	382	14	US-10-225-567A-237	Sequence 237, App	990	70.5	5.9	228	13	US-10-051-903-16	Sequence 16, Appl1
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924	71.5	6.0	405	15	US-10-424-599-149141	Sequence 149141, A	997	70.5	5.9	363	16	US-10-768-878-9	Sequence 9, Appl1
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926	71.5	6.0	433	16	US-10-437-963-156065	Sequence 156065, A	999	70.5	5.9	366	10	US-10-354-247-32	Sequence 32, Appl1
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929	71.5	6.0	524	15	US-10-424-599-248196	Sequence 248196, A	1002	70.5	5.9	374	14	US-10-060-902-30	Sequence 30, Appl1
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932	71.5	6.0	603	15	US-10-382-122A-44316	Sequence 44316, A	1005	70.5	5.9	388	15	US-10-354-247-16	Sequence 16, Appl1
933	71.5	6.0	689	10	US-09-371-347-48	Sequence 48, Appl1	1006	70.5	5.9	390	14	US-10-060-902-22	Sequence 22, Appl1
934	71.5	6.0	697	10	US-09-371-347-46	Sequence 46, Appl1	1007	70.5	5.9	390	14	US-10-060-902-24	Sequence 24, Appl1
935	71.5	6.0	698	10	US-09-371-347-2	Sequence 2, Appl1	1008	70.5	5.9	390	15	US-10-354-247-22	Sequence 22, Appl1
936	71.5	6.0	698	10	US-09-371-347-21	Sequence 21, Appl1	1009	70.5	5.9	390	15	US-10-354-247-24	Sequence 24, Appl1
937	71.5	6.0	698	10	US-09-371-347-42	Sequence 42, Appl1	1010	70.5	5.9	393	14	US-10-060-902-28	Sequence 28, Appl1
938	71.5	6.0	698	10	US-09-371-347-44	Sequence 44, Appl1	1011	70.5	5.9	393	14	US-10-060-902-36	Sequence 36, Appl1
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942	71.5	6.0	2560	15	US-10-276-774-1774	Sequence 1774, Ap	1015	70.5	5.9	402	15	US-10-060-902-34	Sequence 34, Appl1
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947	71.5	6.0	2923	15	US-10-120-801-53	Sequence 53, Appl1	1020	70.5	5.9	407	15	US-10-354-247-26	Sequence 26, Appl1
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954	71	5.9	309	15	US-10-425-114-36801	Sequence 36801, A	1027	70.5	5.9	407	15	US-10-051-903-26	Sequence 26, Appl1
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958	71	5.9	444	15	US-10-287-226-372	Sequence 372, App	1031	70.5	5.9	407	15	US-10-369-493-5442	Sequence 5442, Ap
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1048	70	5.9	333	15	US-10-433-561-32	Sequence 32, App	1121	69	5.8	388	15	US-10-282-122A-42742	Sequence 42742, A
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1059	70	5.9	475	15	US-10-297-022-24	Sequence 24, App	1132	69	5.8	1133	16	US-10-437-963-189159	Sequence 189159, A
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1198	68	5.7	258	14	US-10-023-171-7	Sequence 7, Appl1	1271	68	5.7	488	14	US-10-225-550-296	Sequence 296, App
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1226	68	5.7	346	15	US-10-369-405-30	Sequence 30, Appl	1299	68	5.7	519	16	US-10-115-571A-6	Sequence 6, Appl1
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1231	68	5.7	346	15	US-10-297-247-2	Sequence 2, Appl1	1304	68	5.7	519	16	US-10-437-963-159513	Sequence 159513,
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1235	68	5.7	346	16	US-10-314-048A-88	Sequence 88, Appl	1308	68	5.7	519	16	US-10-932-004-18	Sequence 18, Appl
1236	68	5.7	346	16	US-10-157-262-40	Sequence 40, Appl	1309	68	5.7	519	16	US-09-765-994-4	Sequence 4, Appl1
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1242	68	5.7	355	9	US-09-961-068-1	Sequence 1, Appl1	1315	68	5.7	519	16	US-10-225-567A-607	Sequence 607, App
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1246	68	5.7	355	14	US-10-339-423-62	Sequence 62, Appl	1319	68	5.7	519	16	US-10-407-079-84	Sequence 84, Appl
1247	68	5.7	355	14	US-10-225-567A-62	Sequence 62, Appl	1320	68	5.7	519	16	US-10-698-959-2	Sequence 2, Appl1
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1250	68	5.7	355	14	US-10-339-423-62	Sequence 62, Appl	1323	68	5.7	519	16	US-09-944-045-2	Sequence 2, Appl1
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